

Network Systems
Science & Advanced
Computing
Biocomplexity Institute
& Initiative
University of Virginia

Estimation of COVID-19 Impact in Virginia

April 14th, 2021

(data current to April 10rd – April 13th)

Biocomplexity Institute Technical report: TR 2021-043



BIOCOMPLEXITY INSTITUTE

biocomplexity.virginia.edu

About Us

- Biocomplexity Institute at the University of Virginia
 - Using big data and simulations to understand massively interactive systems and solve societal problems
- Over 20 years of crafting and analyzing infectious disease models
 - Pandemic response for Influenza, Ebola, Zika, and others



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Overview

- **Goal:** Understand impact of COVID-19 mitigations in Virginia
- **Approach:**
 - Calibrate explanatory mechanistic model to observed cases
 - Project based on scenarios for next 4 months
 - Consider a range of possible mitigation effects in "what-if" scenarios
- **Outcomes:**
 - Ill, Confirmed, Hospitalized, ICU, Ventilated, Death
 - Geographic spread over time, case counts, healthcare burdens

Key Takeaways

Projecting future cases precisely is impossible and unnecessary.

Even without perfect projections, we can confidently draw conclusions:

- **Case rates in Virginia have flattened with mix of growth and decline across districts**
- VA mean weekly incidence up to 19/100K from 16/100K, US up (21 from 19 per 100K)
- Progress remains stalled, with most counties at levels 2x the mean rate of Summer 2020
- Projections show slow growth overall across Commonwealth, boosted by B.1.1.7, but curtailed by vaccine
- Recent updates:
 - Modeled age-specific vaccinations past and future as well as severity of B.1.1.7 to drive outcome projections
 - Hospitalizations and deaths **reduced** by vaccination in ages most at risk for severe outcomes, but **increased** by prevalence of B.1.1.7
 - Scenarios adjusted to reflect increasing dominance of B.1.1.7 and return of the Best of Past control scenario
 - Regional vaccine acceptance integrated into projections
- The situation continues to change. Models continue to be updated regularly.

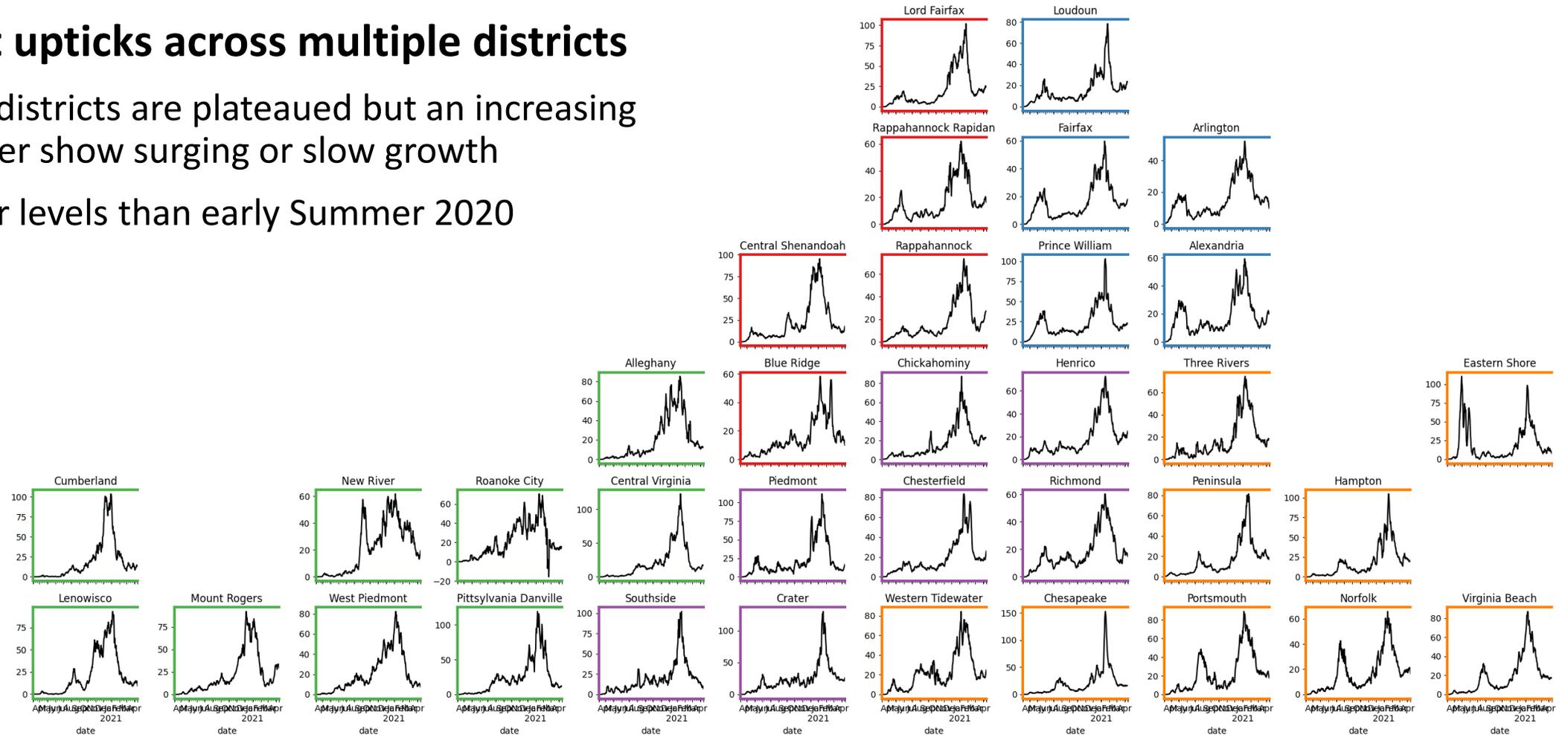
Situation Assessment



Case Rate (per 100k) by VDH District

Recent upticks across multiple districts

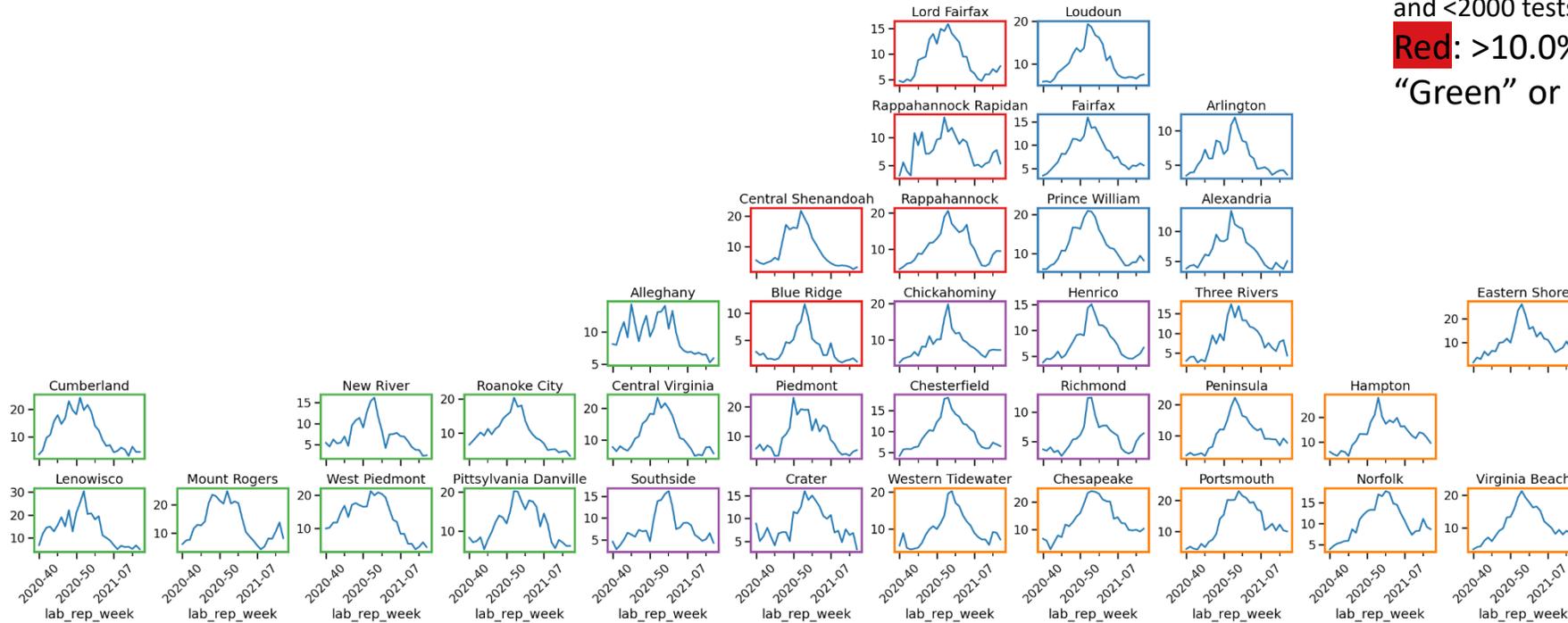
- Most districts are plateaued but an increasing number show surging or slow growth
- Higher levels than early Summer 2020



Test Positivity by VDH District

Weekly changes in test positivity by district

- Some upticks/flattening in the positivity rates
- Nearly 75% of counties still in Red or Yellow categories

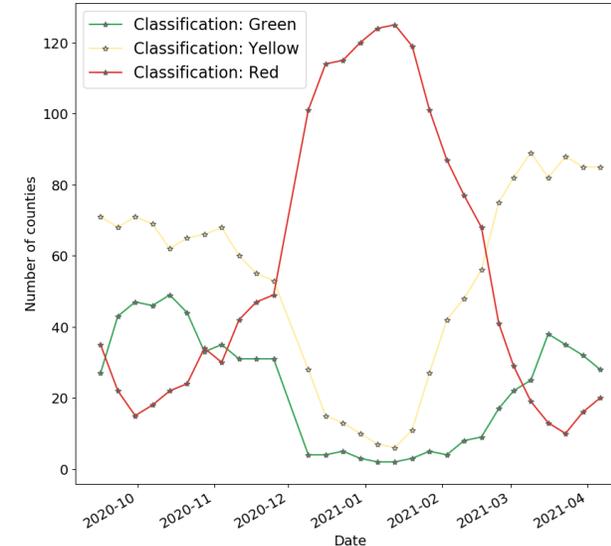


County level test positivity rates for RT-PCR tests.

Green: Test positivity <5.0%
(or with <20 tests in past 14 days)

Yellow: Test positivity 5.0%-10.0% (or with <500 tests and <2000 tests/100k and >10% positivity over 14 days)

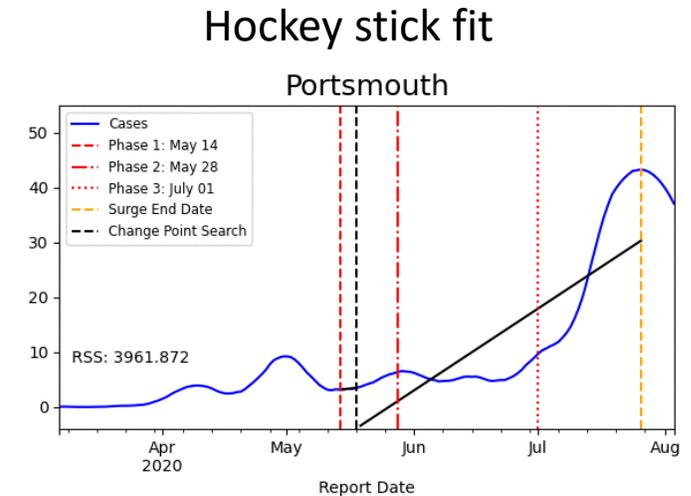
Red: >10.0% and not meeting the criteria for "Green" or "Yellow"



District Trajectories

Goal: Define epochs of a Health District's COVID-19 incidence to characterize the current trajectory

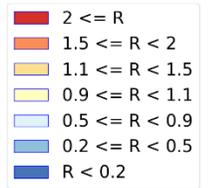
Method: Find recent peak and use hockey stick fit to find inflection point afterwards, then use this period's slope to define the trajectory



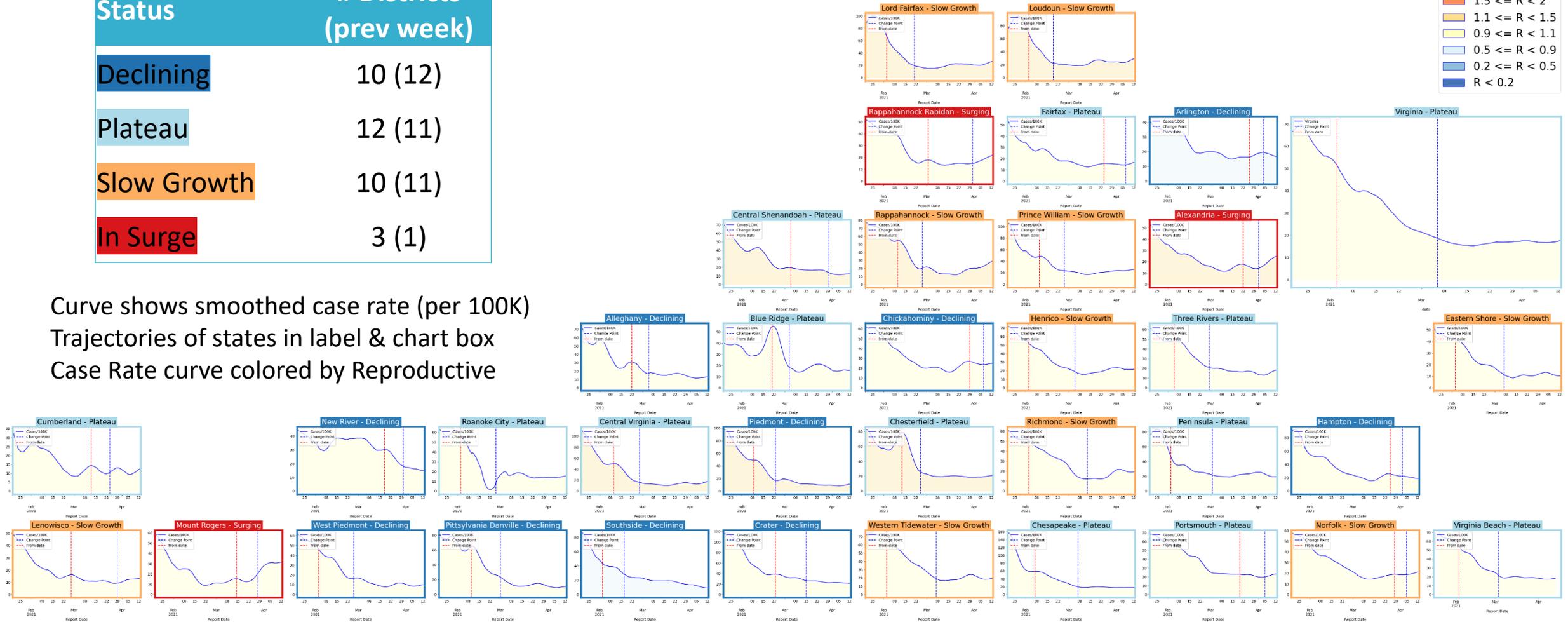
Trajectory	Description	Weekly Case Rate (per 100K) bounds	# Districts (prev week)
Declining	Sustained decreases following a recent peak	below -0.9	10 (12)
Plateau	Steady level with minimal trend up or down	above -0.9 and below 0.5	12 (11)
Slow Growth	Sustained growth not rapid enough to be considered a Surge	above 0.5 and below 2.5	10 (11)
In Surge	Currently experiencing sustained rapid and significant growth	2.5 or greater	3 (1)

District Trajectories – last 10 weeks

Status	# Districts (prev week)
Declining	10 (12)
Plateau	12 (11)
Slow Growth	10 (11)
In Surge	3 (1)



Curve shows smoothed case rate (per 100K)
 Trajectories of states in label & chart box
 Case Rate curve colored by Reproductive



SARS-CoV2 Variants of Concern

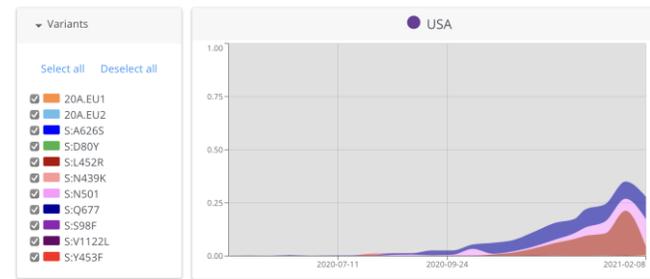
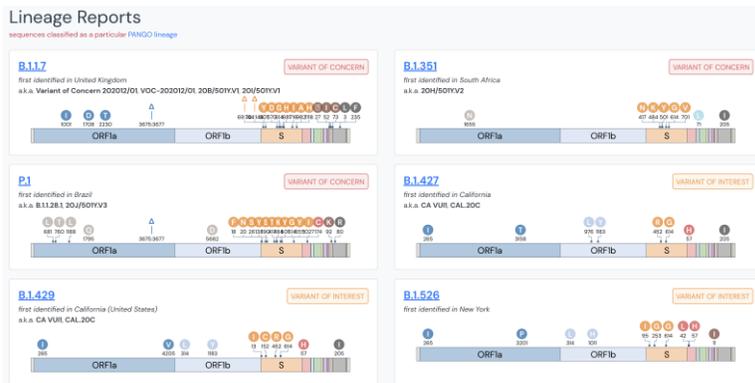
Emerging new variants will alter the future trajectories of pandemic and have implications for future control

- Current evidence supports that new variants can:
 - Increase transmissibility
 - Increase severity (more hospitalizations and/or deaths)
 - Limit immunity provided by prior infection and vaccinations
- Genomic surveillance remains very limited
 - Challenges ability to estimate impact in US to date and estimation of arrival and potential impact in future
 - B.1.1.7 is most frequent and well-studied

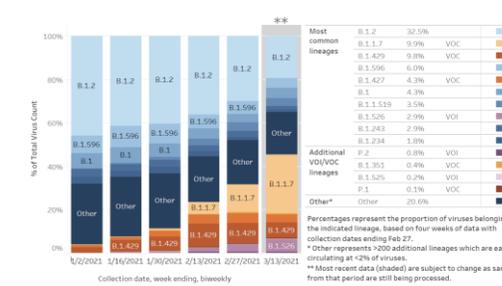
Lineages Of Concern

LoC name	PANGO lineage	NextStrain lineage	Other synonyms	Emergence date	Emergence location	Key AA substitutions in spike protein	Impact
B.1.1.7	B.1.1.7	20I/501Y.V1	VOC 202012/01, UK variant	September 2020	Southeast England	H69-, V70-, N501Y, D614G, P681H	Increased transmissibility; S gene target failure (SGTF)
B.1.351	B.1.351	20H/501Y.V2	South African variant	October 2020	Nelson Mandela Bay, South African	L241-, L242-, A243-, K417N, E484K, N501Y, D614G	loss of serum antibody neutralization
P.1	B.1.1.28	20J/501Y.V3	Brazilian variant	July 2020	Brazil	K417T, E484K, N501Y, D614G	Increased transmissibility; loss of serum antibody neutralization
CAL.20C	B.1.429			July 2020	Southern California, USA	W152C, L452R, D614G	loss of monoclonal antibody binding
B.1.375	B.1.375			September 2020	Massachusetts, USA	H69-, V70-, D614G	S gene target failure (SGTF)

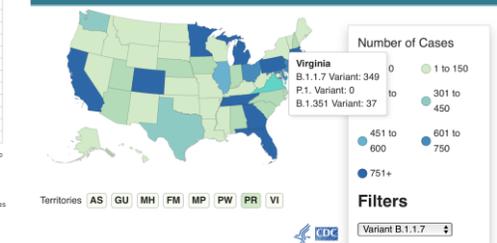
[NIH-NIAID Bacterial-Viral Bioinformatics Resource Center](#)



SARS-CoV-2 Variants Circulating in the United States



Variant	Reported Cases	Jurisdictions
B.1.1.7	20,915	52
B.1.351	453	36
P.1	497	31



[outbreak.info](#)

[Outbreak Info](#)

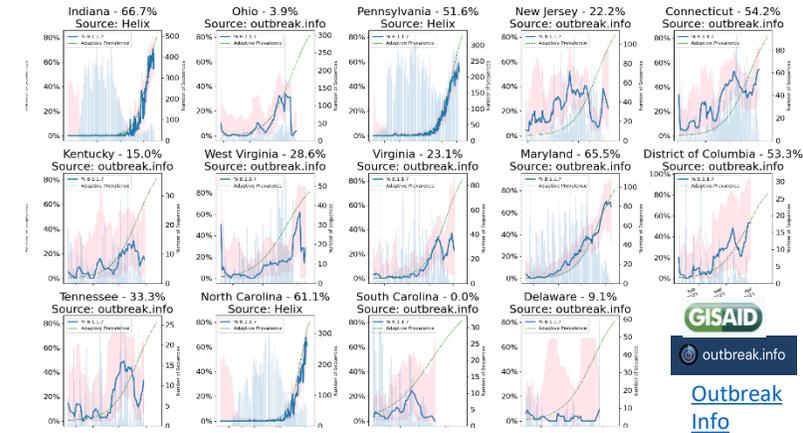
[CoVariants](#) [CoVariants.org](#)

[CDC](#) [CDC Variant Tracking](#)

SARS-CoV2 Variants of Concern

Lineage B.1.1.7

- B.1.1.7 has been detected in Virginia and has continued to rapidly grow though has been hard to track. Current estimates suggest VA may be at 23% (while nationally CDC has said it has reached 50%, while the same data source reports frequency at 37%), however, these estimates fluctuate significantly.



Transmissibility:

- [Science](#) study using two-strain model supports that increased transmissibility, duration of infectiousness, or increased transmission in children best fit the epi data observed in the UK across regions. Some combination of all also likely.
- [Study from Public Health England](#) shows contacts of B.1.1.7 cases are more likely (50%) to test positive than contacts of non-B.1.1.7 patients
- [Study](#) shows B.1.1.7 patients have longer periods of infection

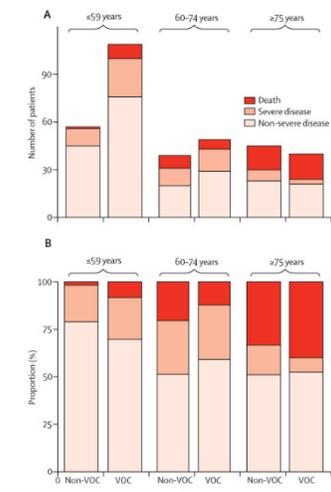
Severity:

- [Evidence](#) continues [to mount](#) supporting increased risks of hospitalization B.1.1.7 infected individuals
- [Danish](#) study shows B.1.1.7 to have a 64% higher risk of hospitalization, while [Public Health Scotland](#) studies showed a range of 40% to 60%
- [Study in Nature](#) based on UK data estimates B.1.1.7 cases have 60% higher mortality
- [Sequence based study in Lancet](#), contradicts these findings and found no association with severity and death from B.1.1.7 infections

Table 1 | Absolute 28-day mortality risk associated with B.1.1.7, as expressed by case fatality ratio (%) among individuals testing positive in the community

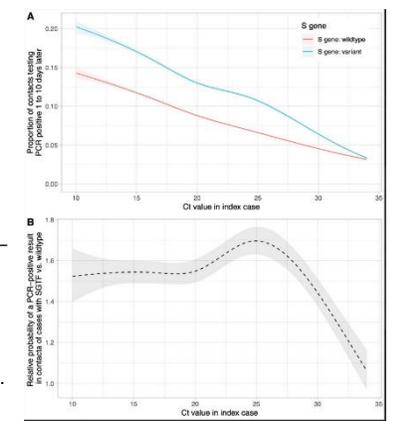
Sex	Age	Baseline	SGTF, complete cases	p_{adj} IPW
Female	0-34	0.00069%	0.0011% (0.00096-0.0012%)	0.0011% (0.00097-0.0012%)
	35-54	0.033%	0.050% (0.045-0.056%)	0.052% (0.046-0.059%)
	55-69	0.18%	0.28% (0.25-0.31%)	0.29% (0.26-0.33%)
	70-84	2.9%	4.4% (4.0-4.9%)	4.6% (4.0-5.1%)
	85 and older	13%	19% (17-21%)	20% (18-22%)
Male	0-34	0.0031%	0.0047% (0.0042-0.0052%)	0.0049% (0.0043-0.0055%)
	35-54	0.064%	0.099% (0.089-0.11%)	0.10% (0.090-0.12%)
	55-69	0.56%	0.86% (0.77-0.95%)	0.89% (0.78-1.0%)
	70-84	4.7%	7.2% (6.4-7.9%)	7.4% (6.6-8.3%)
	85 and older	17%	25% (23-27%)	26% (23-29%)

The baseline risk (i.e., for preexisting SARS-CoV-2 variants) is derived using linked deaths within 28 days for all individuals testing positive in the community from 1 August - 31 October 2020. Adjusted risks are presented for the SGTF analysis for complete cases and for the misclassification-adjusted (p_{adj}) IPW analysis, which yielded the lowest and highest mortality estimates, respectively, of the main models assessed (Fig. 2a-d).



Of 496 patients with samples positive for SARS-CoV-2 on PCR and who met inclusion criteria, 341 had samples that could be sequenced. 198 (58%) of 341 had B.1.1.7 infection and 143 (42%) had non-B.1.1.7 infection. We found no evidence of an association between severe disease and death and lineage (B.1.1.7 vs non-B.1.1.7) [Lancet](#)

PCR testing in England from Sept 2020 - Feb 2021 combined with contact tracing data found B.1.1.7 cases to have higher viral loads (based on PCR cycle thresholds) and increased likelihood of causing infections among contacts. B.1.1.7 increased transmission by ~50%. [Medrxiv](#)



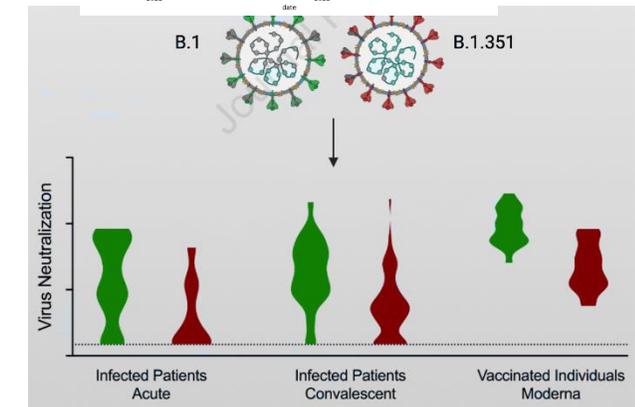
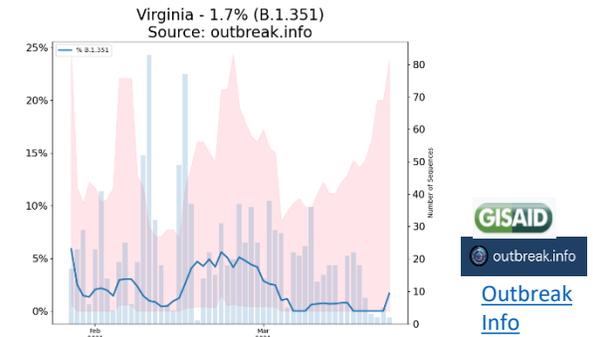
SARS-CoV2 Variants of Concern

Lineage B.1.351

- Emerging strain initially identified in South Africa shows signs of vaccine escape, currently 452 reported cases in 36 states (including 37 now in Virginia)

Immune Escape:

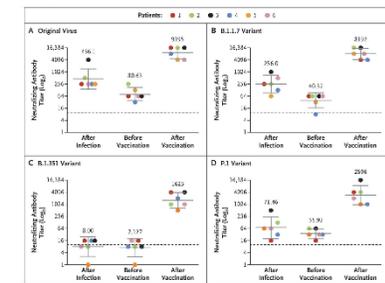
- Many studies show that convalescent sera from previously infected individuals does not neutralize B.1.351 virus well, however, vaccine induced immunity shows signs of effectiveness
- [One study](#) supports [a previous study](#) based on clinical trial data showing that convalescent serum neutralization is highly predictive of actual immune protection for infection
- [Another study in Cell](#) supports [previous report](#) demonstrating that despite reduced antibody binding, the Moderna vaccinated individuals able to neutralize the B.1.351 variant
- [New England Journal Study](#) shows that people with prior infections who are then vaccinated (one dose of Pfizer) the boosted immunity is effective against B.1.351
- Some [evidence emerging](#) that variants like B.1.351 may be more likely to cause secondary infections after vaccination. As more of the population is protected we may find B.1.351 and other immune evading variants becoming more prevalent.



Despite reduced antibody binding to the B.1.351 RBD, sera from infected (acute and convalescent) and Moderna (mRNA-1273) vaccinated individuals were still able to neutralize the SARS-CoV-2 B.1.351 variant. [Cell](#)

	B.1.1.7		B.1.351	
	Case	Control	Case	Control
Full effectiveness	128	6	0	0
	4	2	1	140
Partial effectiveness	195	28	0	1
	10	14	1	245

Small Case control study suggests that among those infected after their 1st and 2nd dose, they are more likely to be B.1.351 in the earlier infections, and B.1.1.7 in the later breakthrough infections. [Medrxiv](#)



Six patients previously infected with the original virus received the BNT162b2 vaccine. Before vaccination, they had neutralizing activity against the B.1.1.7 and P.1 variants but not B.1.351. After one dose, neutralizing activity against all variants increased greatly. [NEJM](#)

SARS-CoV2 Variants of Concern

Lineage P.1

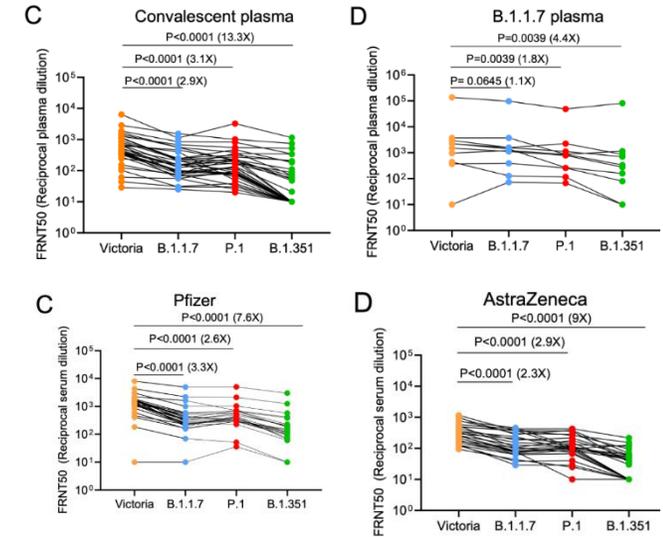
- Present in at least 172 cases in 22 states, shows signs of increased transmissibility and ability to evade immunity
- Caused a [resurgence of hospitalizations in Manaus, Brazil](#) which has now caused more deaths in last 3 months than all of 2020
- Study in [Cell](#) shows P.1 may be less resistant to neutralization than B.1.351

Lineage B.1.429

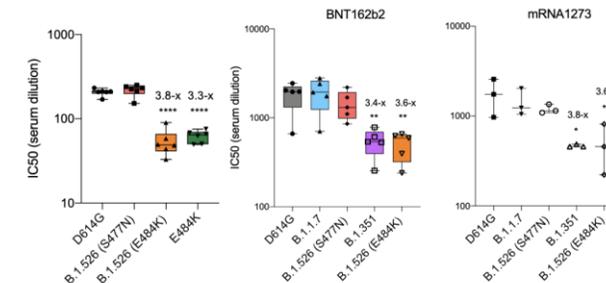
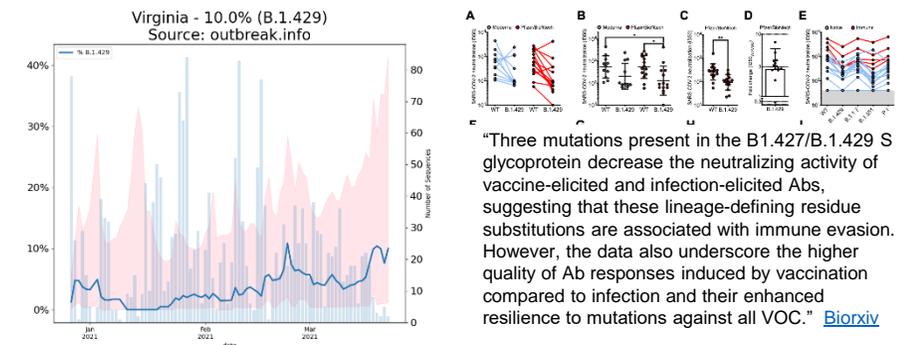
- Recently officially recognized as variant of concern, estimates of ~20% increase in transmission and some evasion of immunity
- Initially found in Southern California, coincided with surge in Nov and Dec, [found in over half of sequenced samples in LA](#)

Lineage B.1.526

- Initially identified in NY and found increasingly as cases in NY / NJ increase
- Recent study finds vaccine-elicited plasma neutralizes B.1.526 but less efficiently than other variants



P.1 and B.1.351 having a virtually identical triplet: E484K, K417N/T and N501Y, confer similar increased affinity for ACE2. Despite this, P.1 is significantly less resistant to naturally acquired or vaccine induced antibody responses than B.1.351 suggesting that changes outside the RBD impact neutralization. [Cell](#)



B.1.526 SARS-CoV-2 variants identified in New York City are neutralized by vaccine-elicited and therapeutic monoclonal antibodies. [BioRxiv](#)

Estimating Daily Reproductive Number

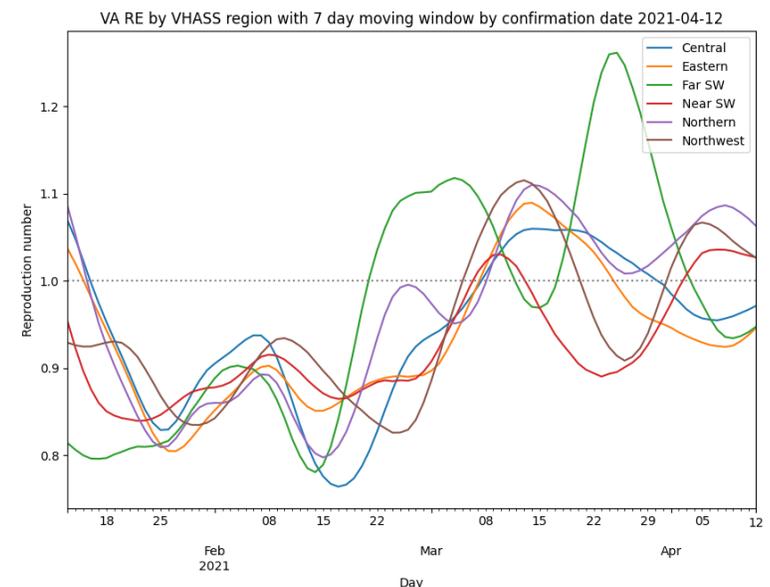
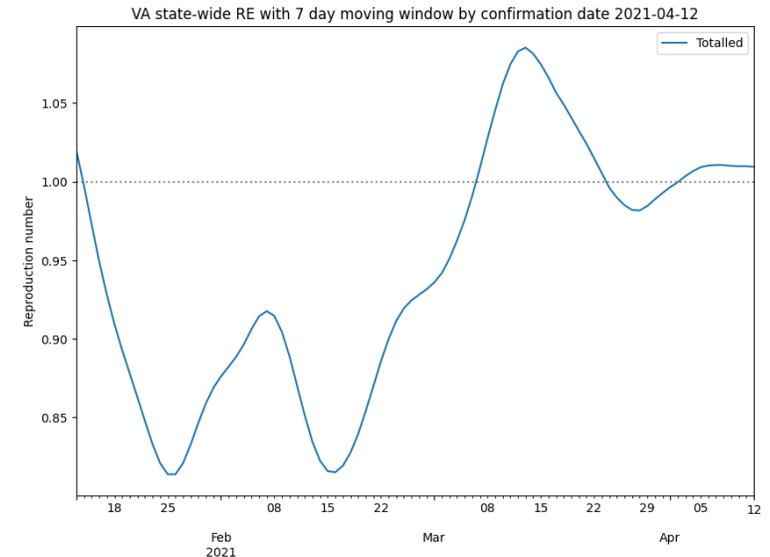
April 12th Estimates

Region	Date Confirmed R_e	Date Confirmed Diff Last Week
State-wide	1.009	0.066
Central	0.971	-0.013
Eastern	0.946	0.026
Far SW	0.947	-0.068
Near SW	1.027	0.156
Northern	1.063	0.085
Northwest	1.026	0.151

Methodology

- Wallinga-Teunis method (EpiEstim¹) for cases by **confirmation date**
- Serial interval: updated to discrete distribution from observations (mean=4.3, Flaxman et al, Nature 2020)
- Using Confirmation date since due to increasingly unstable estimates from onset date due to backfill

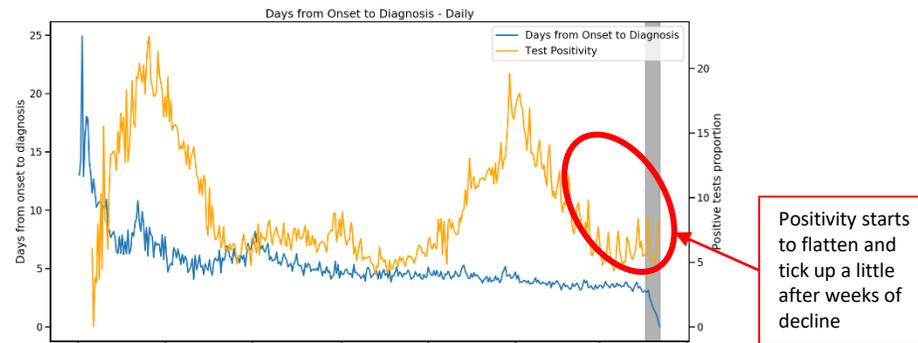
1. Anne Cori, Neil M. Ferguson, Christophe Fraser, Simon Cauchemez. A New Framework and Software to Estimate Time-Varying Reproduction Numbers During Epidemics. American Journal of Epidemiology, Volume 178, Issue 9, 1 November 2013, Pages 1505–1512, <https://doi.org/10.1093/aje/kwt133>



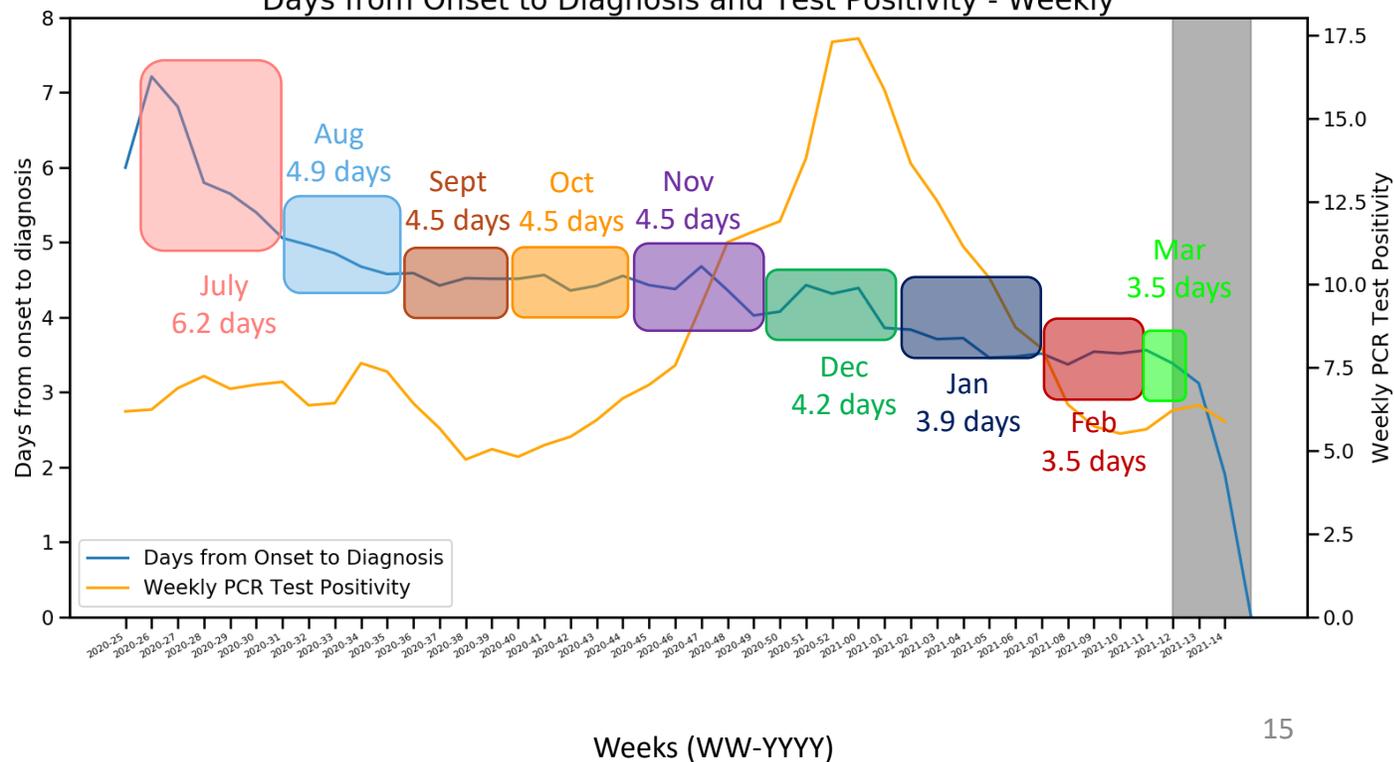
Changes in Case Detection

Timeframe (weeks)	Mean days	% difference from overall mean
July (26-30)	6.2	-4%
Aug (31-34)	4.9	-24%
Sept (35-38)	4.5	-30%
Oct (39-43)	4.5	-31%
Nov (44-47)	4.5	-30%
Dec (48-49)	4.2	-34%
Jan (00-04)	3.9	-40%
Feb (05-08)	3.5	-46%
Mar (09-12)	3.5	-46%
Overall (13-12)	6.5	--

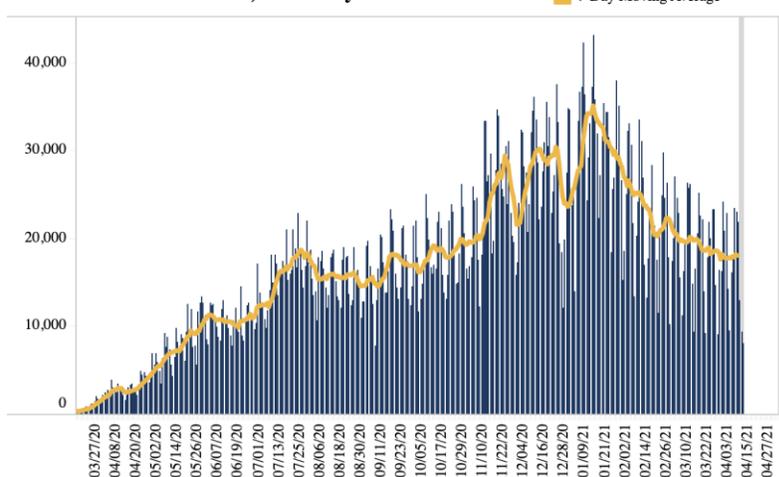
Test positivity vs. Onset to Diagnosis



Days from Onset to Diagnosis and Test Positivity - Weekly

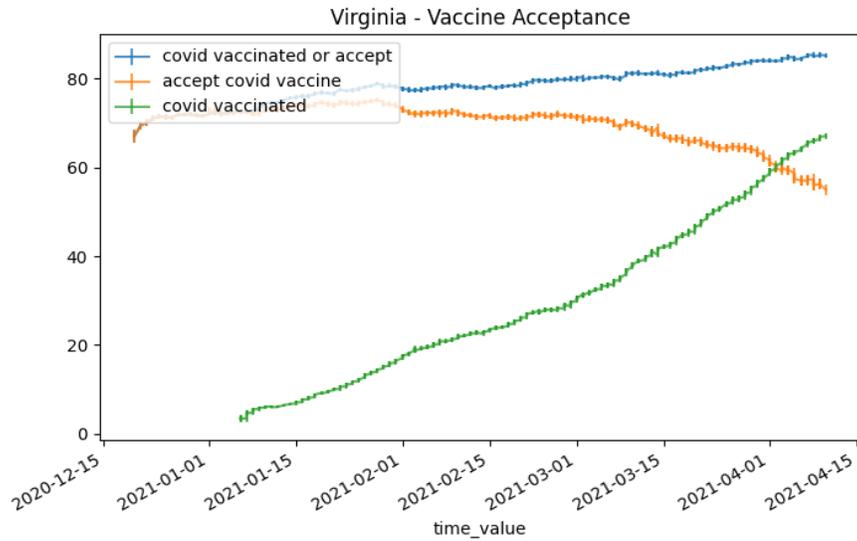


Number of Testing Encounters by Lab Report Date - All Health Districts, PCR Only



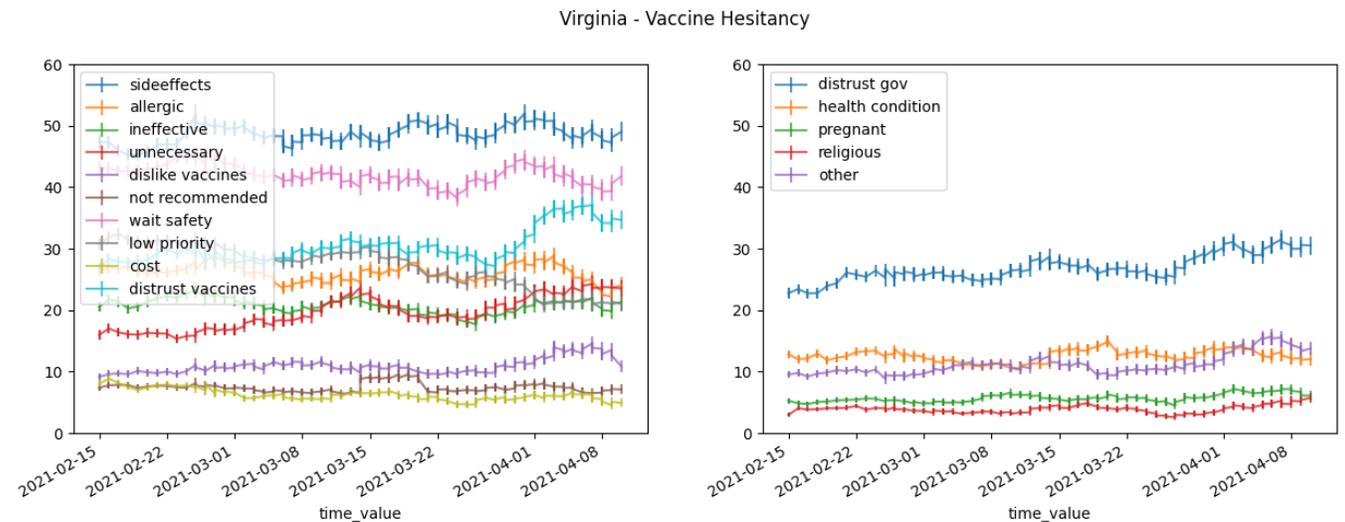
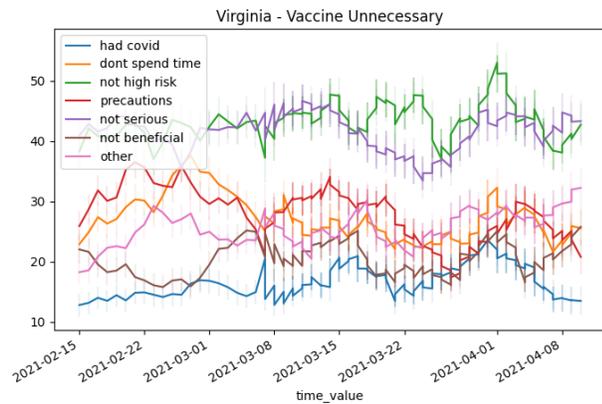
Accessed 8:30am April 14, 2021
<https://www.vdh.virginia.gov/coronavirus/>

Vaccine Acceptance in Virginia



Acceptance remains high:

- Proportion of Virginians that have already or would definitely or probably accept vaccination if offered today
- *Survey respondents are reporting high levels of vaccination of ~50% reflecting some bias of the mechanism*
- Nearly 80% Virginians have already or will choose to be vaccinated
- Top reasons for hesitancy: side effects, safety, distrust (increasing)
- Reasons for unnecessary vaccine: increasing levels of “not serious” disease in past 2 weeks

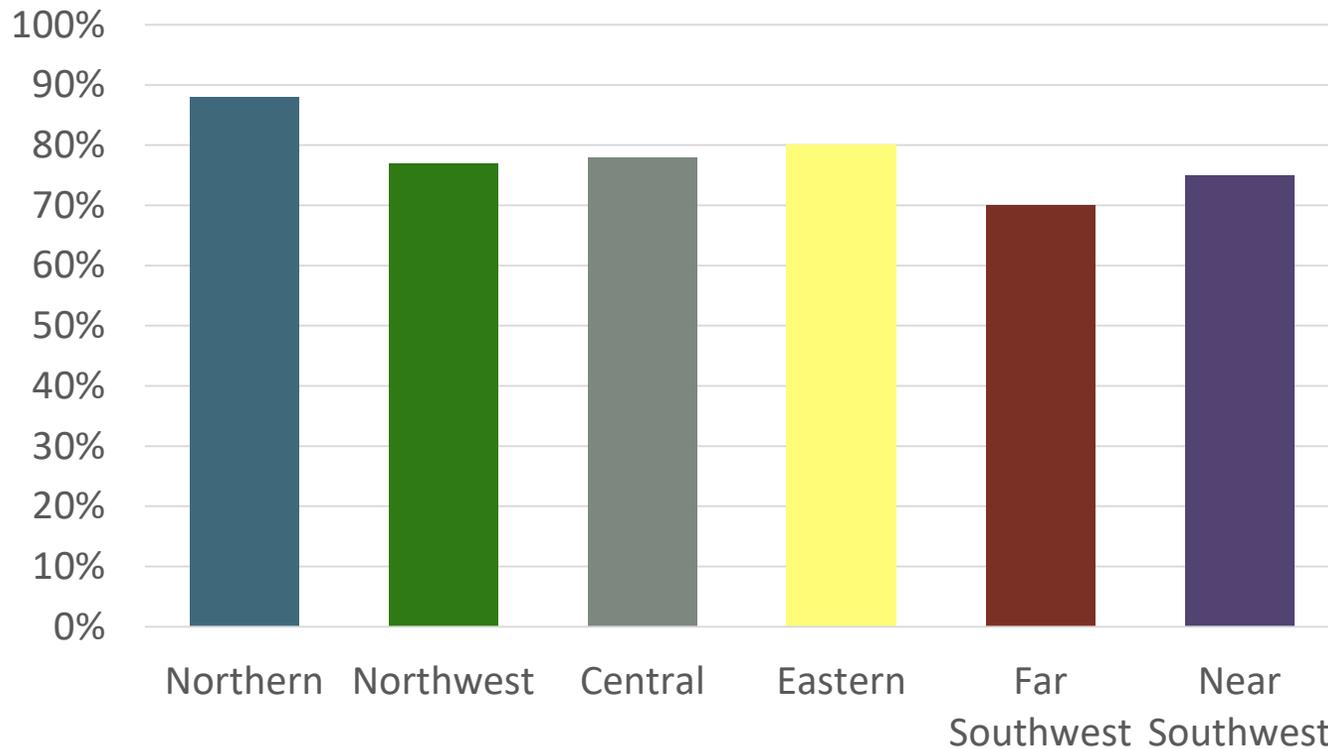


Data Source: <https://covidcast.cmu.edu>

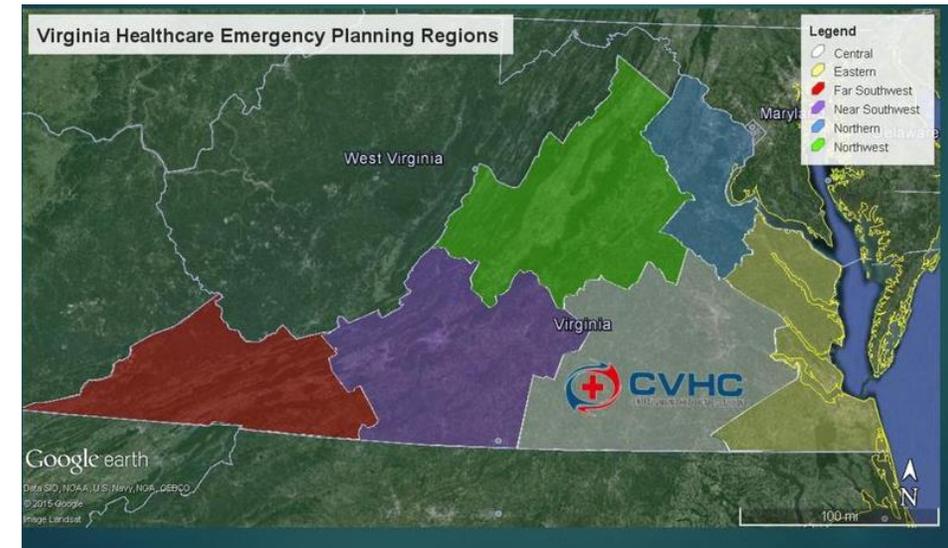


Vaccination Acceptance by Region

Vaccinated Already or Accepting of Vaccine



Virginia Region	Vaccinated Already or Accepting of Vaccine
Northern	88%
Northwest	77%
Central	78%
Eastern	80%
Far Southwest	70%
Near Southwest	75%



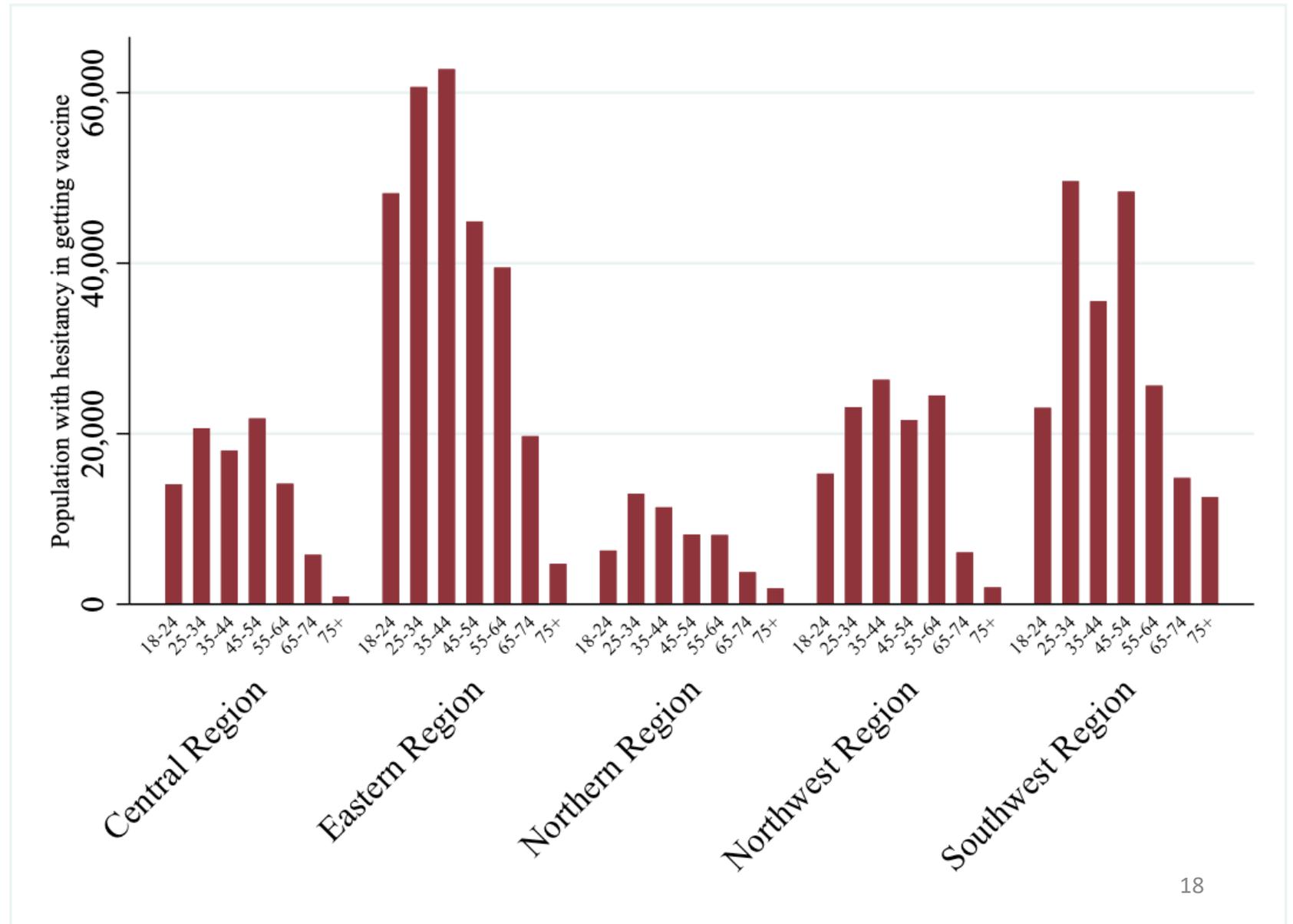
Data Source: <https://covidcast.cmu.edu>



Vaccination Acceptance by Region

Estimated numbers of vaccine hesitant people by age:

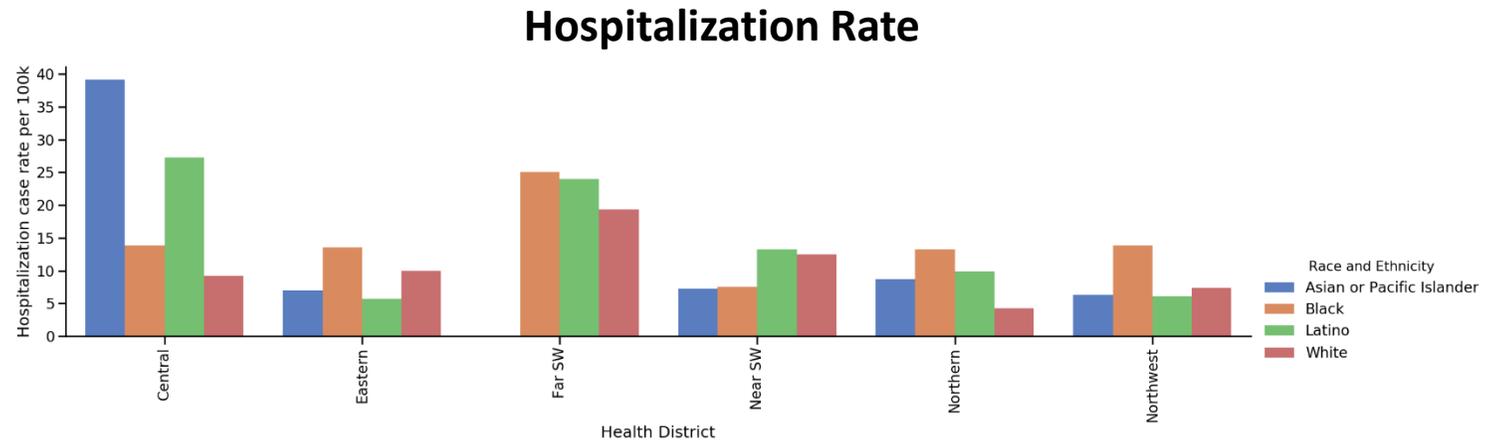
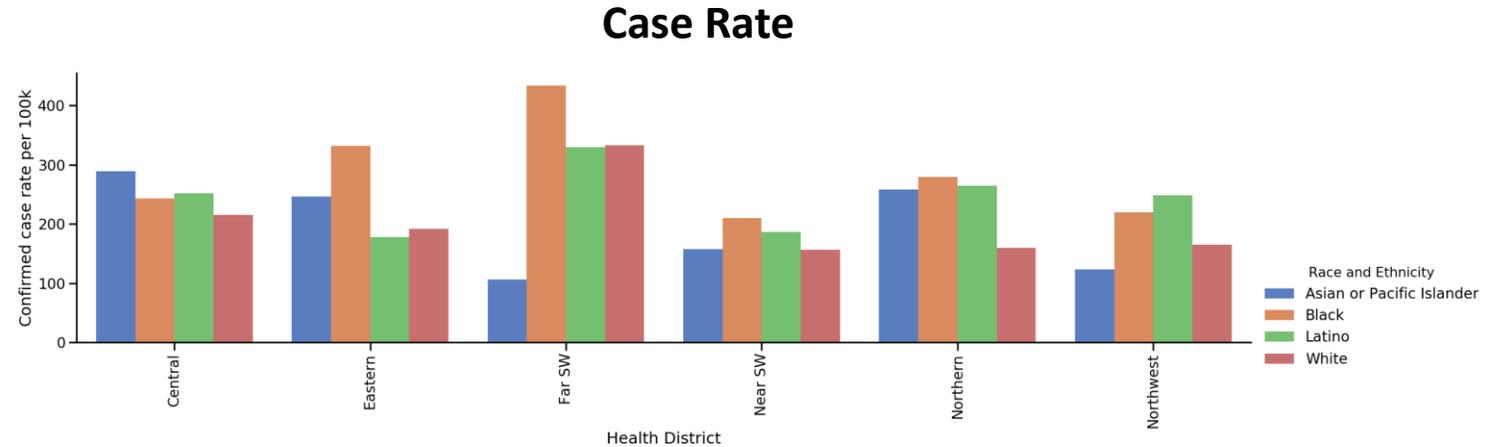
- Even with small population size Southwest has the most hesitant
- Ages 25-55 are most hesitant in these regions
- Pockets of unvaccinated of these sizes can lead to large outbreaks and allow transmission to continue for some time



Race and Ethnicity – Recent Rate Changes (per 100K)

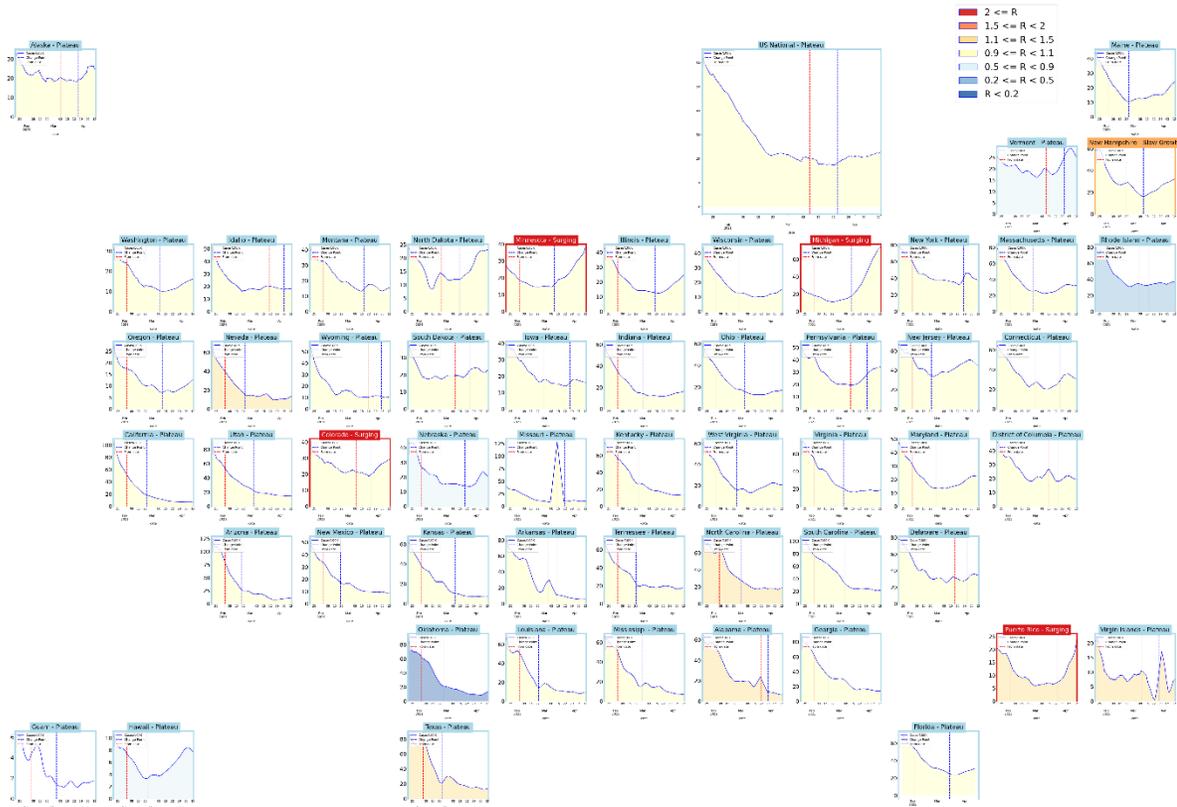
Changes in Race and Ethnicity Rates (per 100k) in past two weeks

- Two week change in population level rates
- Black, Latinx and 2 or more races populations have much higher changes in rates; disparity is more pronounced in some regions than others
- Based on 2019 census race-ethnicity data by county

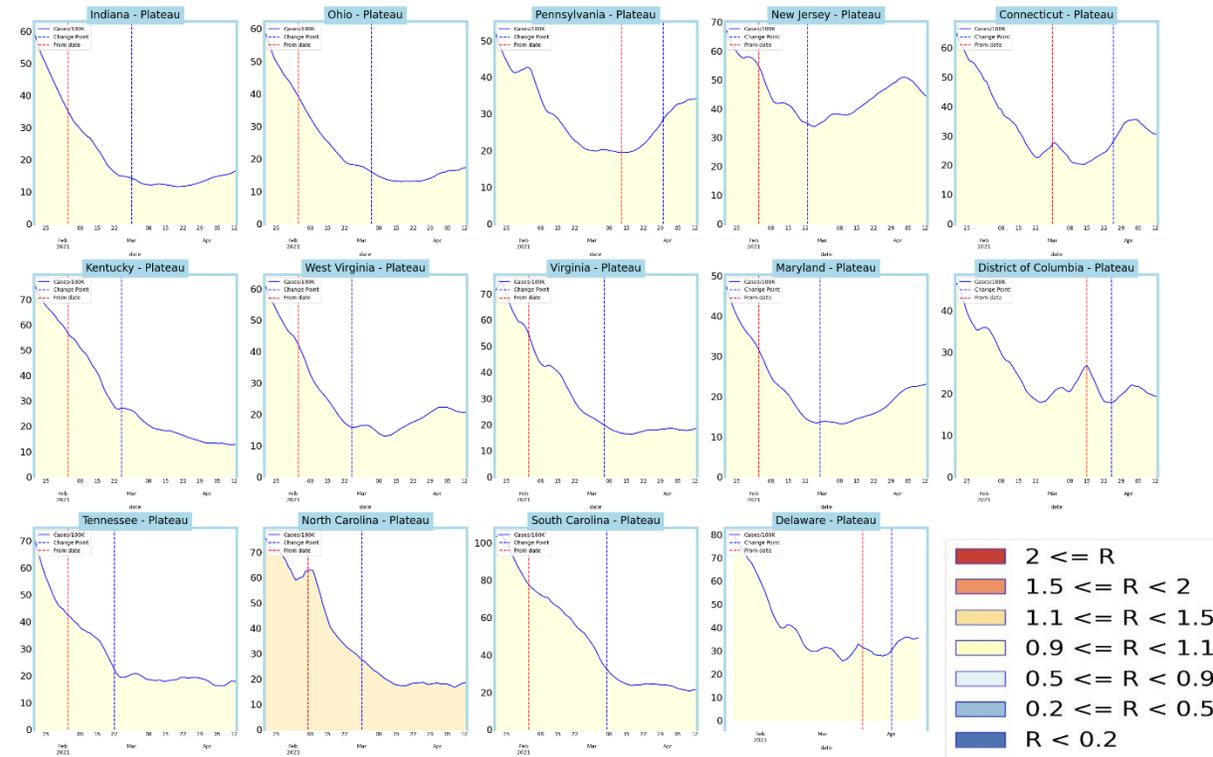


Other State Comparisons

Trajectories of States



Virginia and her neighbors

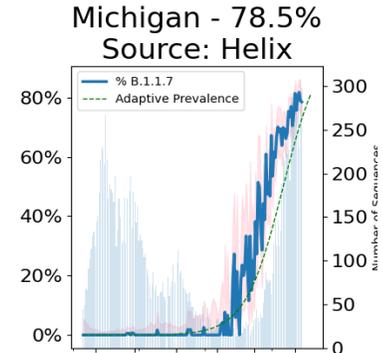
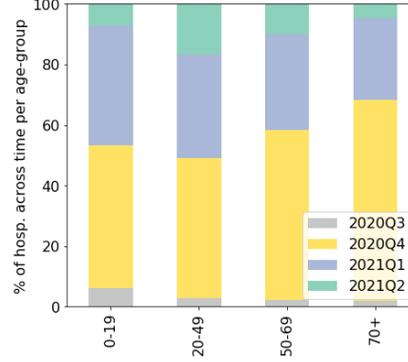
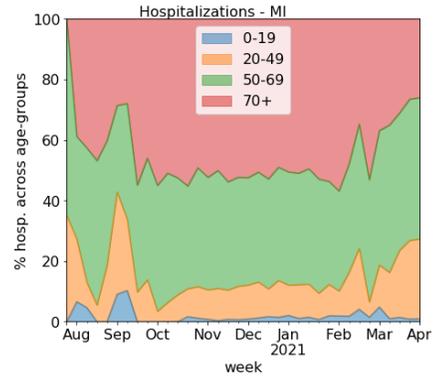
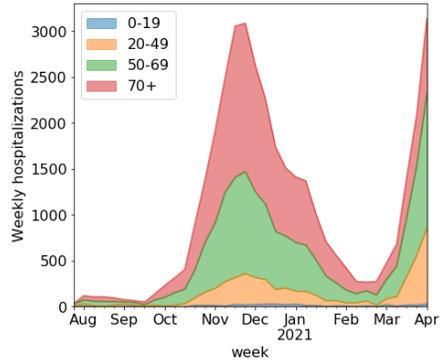


- Nearly all states are plateaued, with 4 jurisdictions now in surge
- Many plateaued states show signs of growth
- Several states experienced short periods of growth but have since slowed / declined

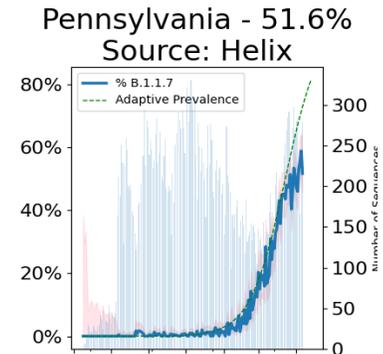
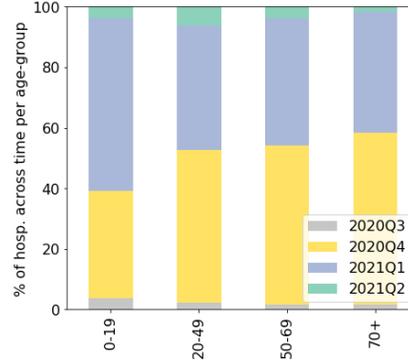
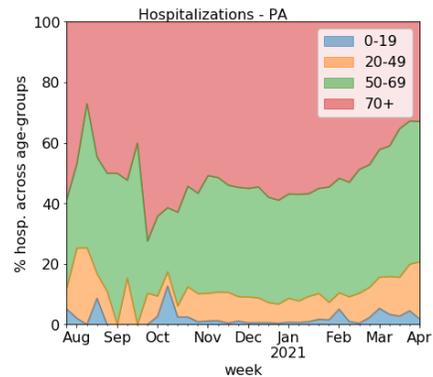
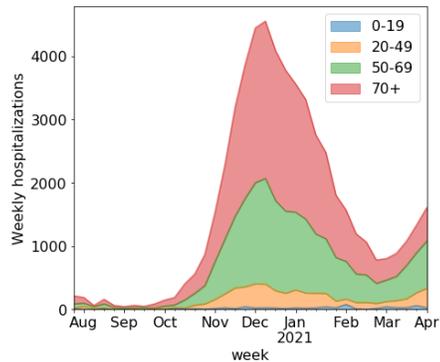
- VA and neighbors are in plateau
- Several neighbors experienced periods of growth but have since leveled off

Other State Comparisons - Hospitalizations

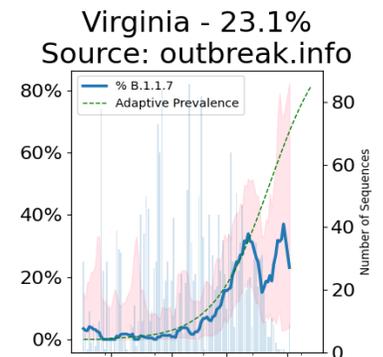
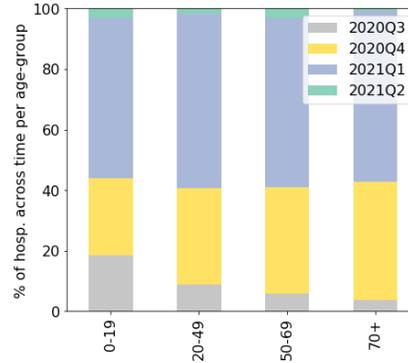
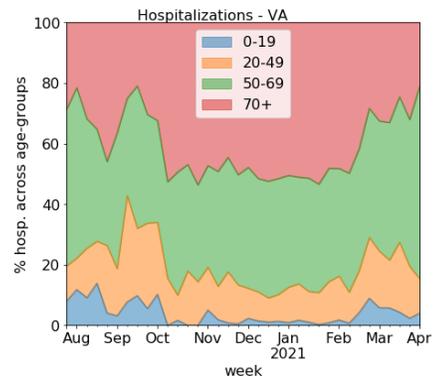
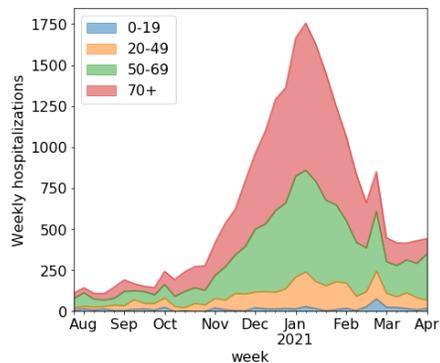
Michigan



Pennsylvania



Virginia



Shifting Age Distribution of cases being hospitalized

- Dual forces of vaccinations in older groups and severity of B.1.1.7 are dramatically shifting the age distribution of hospitalized patients
- Michigan's hospitalizations are rising steeply, consist of more 20-59 year olds
- Pennsylvania lags Michigan, but shows same shift
- Virginia, even more delayed, is likely to follow this pattern as well

Zip code level weekly Case Rate (per 100K)

Case Rates in the last week by zip code

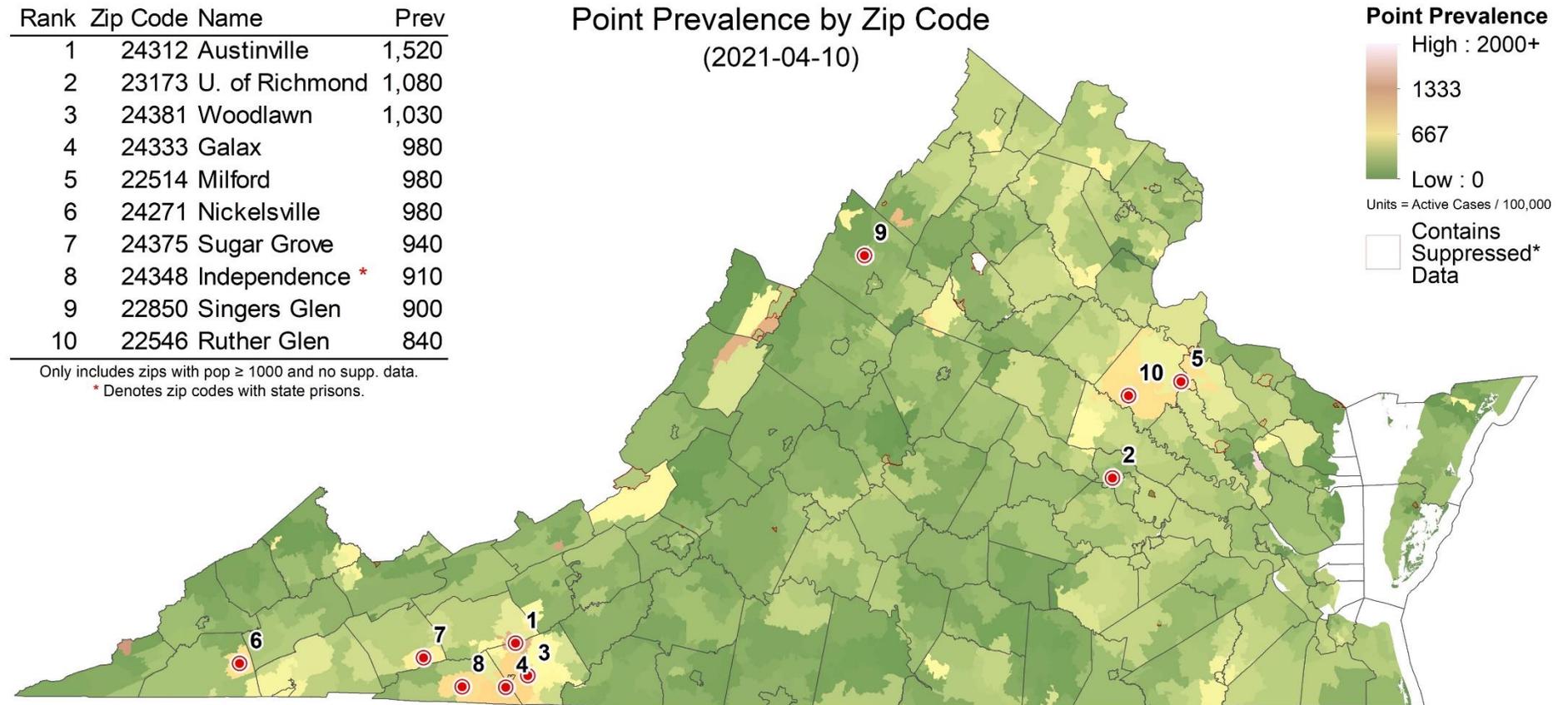
- Concentrations in Southwest, which was preceded by cluster of increased HCW rates last week
- Still some universities in top 10
- Some counts are low and suppressed to protect anonymity, those are shown in white

Rank	Zip Code	Name	Prev
1	24312	Austinville	1,520
2	23173	U. of Richmond	1,080
3	24381	Woodlawn	1,030
4	24333	Galax	980
5	22514	Milford	980
6	24271	Nickelsville	980
7	24375	Sugar Grove	940
8	24348	Independence *	910
9	22850	Singers Glen	900
10	22546	Ruther Glen	840

Only includes zips with pop ≥ 1000 and no supp. data.

* Denotes zip codes with state prisons.

Point Prevalence by Zip Code
(2021-04-10)



Based on Spatial Empirical Bayes smoothed point prevalence for week ending 2021-04-03.

Note: New color ramp scale and new ascertainment ratio of 2:1.

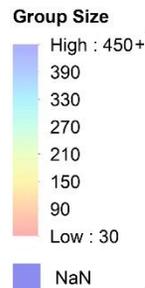
Risk of Exposure by Group Size and HCW prevalence

Case Prevalence in the last week by zip code used to calculate risk of encountering someone infected in a gathering of randomly selected people (group size 25)

- **Group Size:** Assumes 2 undetected infections per confirmed case (ascertainment rate from recent seroprevalence survey), and shows minimum size of a group with a 50% chance an individual is infected by zip code (eg in a group of 23 in Austinville, there is a 50% chance someone will be infected)
- **HCW prevalence:** Case rate among health care workers (HCW) in the last week using patient facing health care workers as the denominator

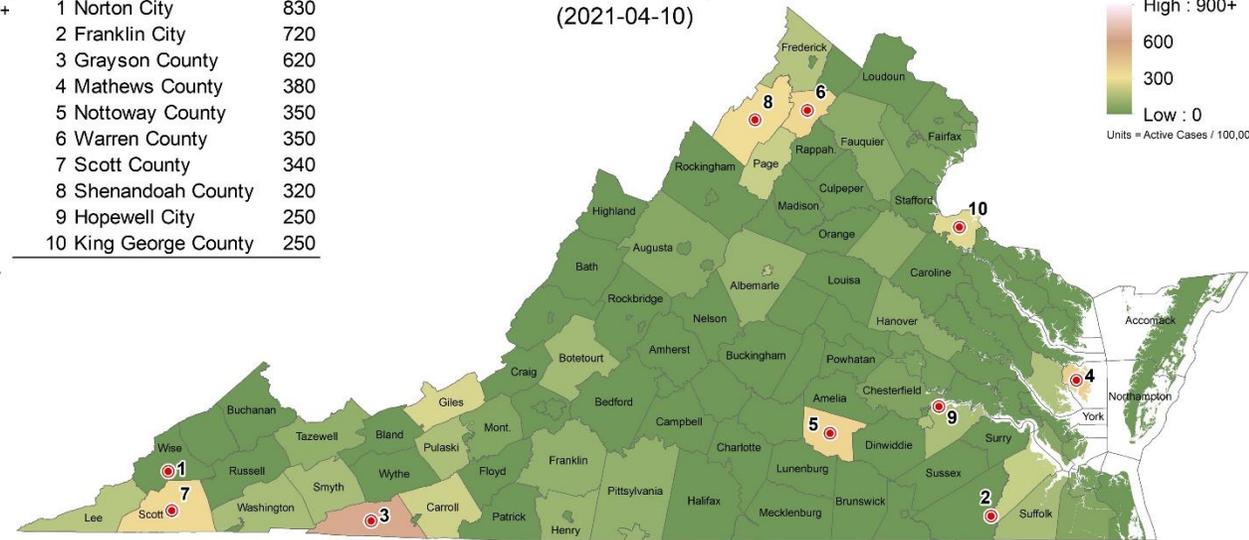
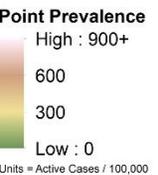
Rank	Zip Code	Name	Size
1	24312	Austinville	23
2	23173	U. of Richmond	26
3	24381	Woodlawn	28
4	24333	Galax	29
5	22514	Milford	29
6	24271	Nickelsville	32
7	24375	Sugar Grove	34
8	24348	Independence *	34
9	22850	Singers Glen	40
10	22546	Ruther Glen	47

Group Size Needed for 50% Likelihood of ≥1 Infected



Rank	Name	Prev
1	Norton City	830
2	Franklin City	720
3	Grayson County	620
4	Mathews County	380
5	Nottoway County	350
6	Warren County	350
7	Scott County	340
8	Shenandoah County	320
9	Hopewell City	250
10	King George County	250

HCW Point Prevalence by Zip Code (2021-04-10)



Note: Scale differs from general public prevalence maps.

Based on Spatial Empirical Bayes smoothed point prevalence for week ending 2021-04-10.
Note: New color ramp scale and new ascertainment ratio of 2:1.

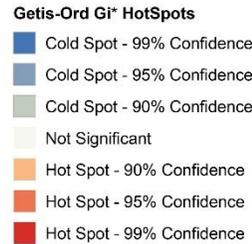
Current Hot-Spots

Case rates that are significantly different from neighboring areas or model projections

- **Spatial:** SaTScan based hot spots compare clusters of zip codes with weekly case prevalence higher than nearby zip codes to identify larger areas with statistically significant deviations
- **Temporal:** The weekly case rate (per 100K) projected last week compared to observed by county, which highlights temporal fluctuations that differ from the model's projections

Spatial Hotspots

Point Prevalence Hot Spots by Zip Code
(2021-04-10)



Spot	Zip Code	Name	Conf.
1	24312	Austinville	99%
2	24333	Galax	99%
3	24381	Woodlawn	99%
4	23173	U. of Richmond	99%
5	22546	Ruther Glen	99%
6	24348	Independence *	99%
7	24271	Nickelsville	99%
8	22514	Milford	99%
9	22580	Woodford	99%
10	24375	Sugar Grove	90%

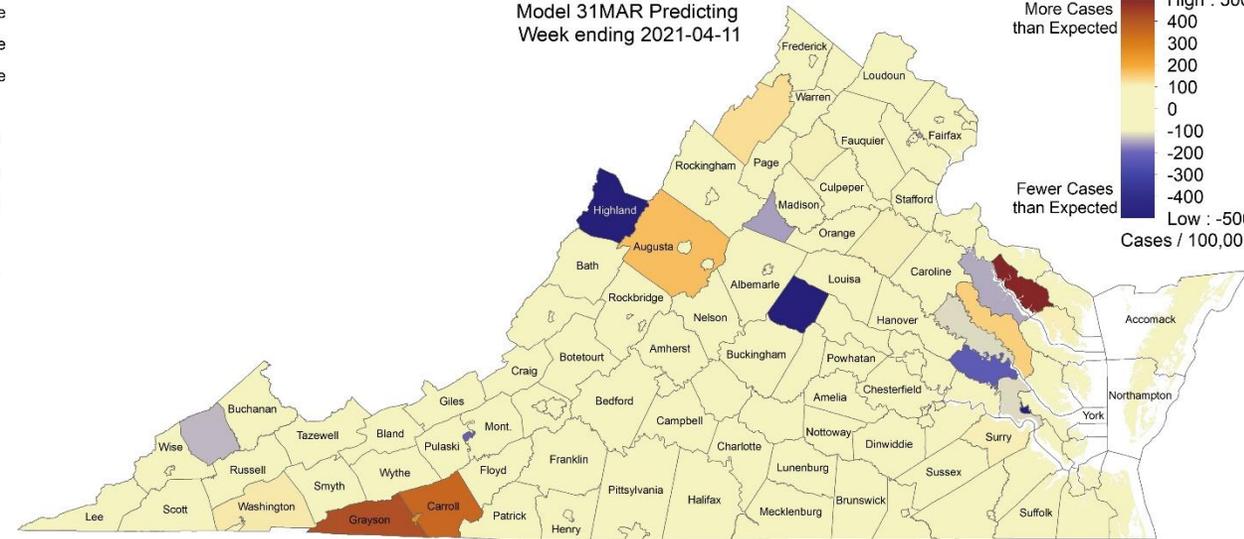
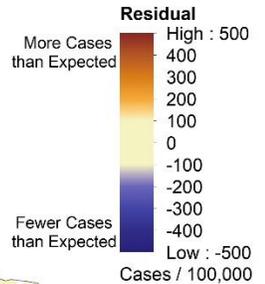
Only includes zips with pop ≥ 1000 and no supp. data.
* Denotes zip codes with state prisons.



Based on Global Empirical Bayes smoothed point prevalence for week ending 2021-04-03.

Temporal Hotspots

Weekly Point Prevalence Model Residuals
Model 31MAR Predicting
Week ending 2021-04-11



Moran's I = 0.044998, Z-Score = 0.688853, P-Value = 0.490916
No Residual Autocorrelation Detected

Model Update – Adaptive Fitting

Adaptive Fitting Approach

Each county fit precisely, with recent trends used for future projection

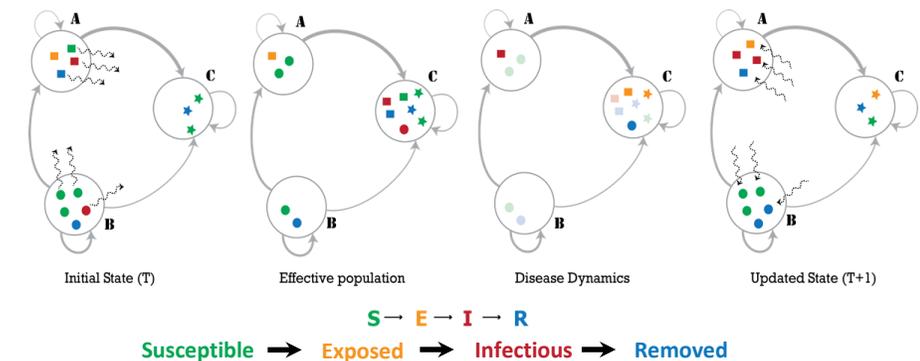
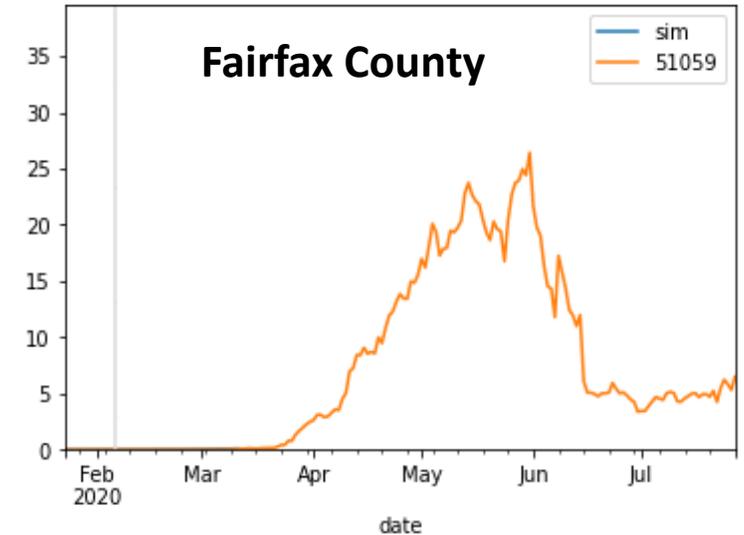
- Allows history to be precisely captured, and used to guide bounds on projections

Model: An alternative use of the same meta-population model, PatchSim

- Allows for future “what-if” Scenarios to be layered on top of calibrated model
- Eliminates connectivity between patches, to allow calibration to capture the increasingly unsynchronized epidemic

External Seeding: Steady low-level importation

- Widespread pandemic eliminates sensitivity to initial conditions
- Uses steady 1 case per 10M population per day external seeding



Using Ensemble Model to Guide Projections

Ensemble methodology that combines the Adaptive with machine learning and statistical models such as:

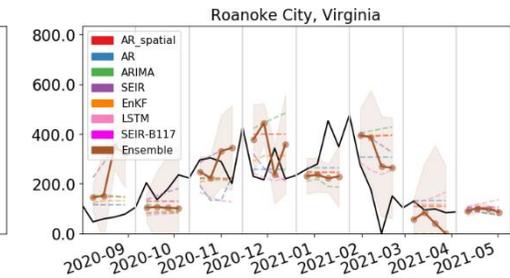
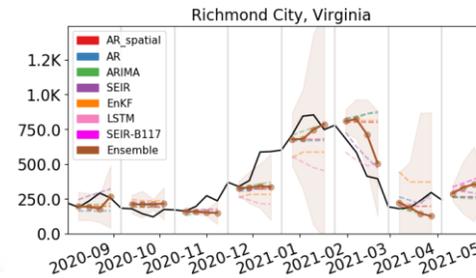
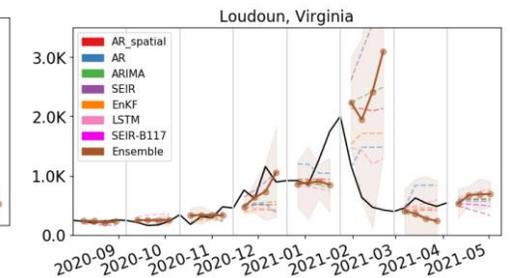
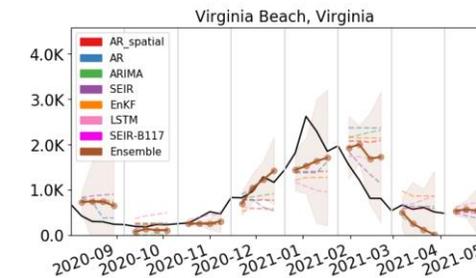
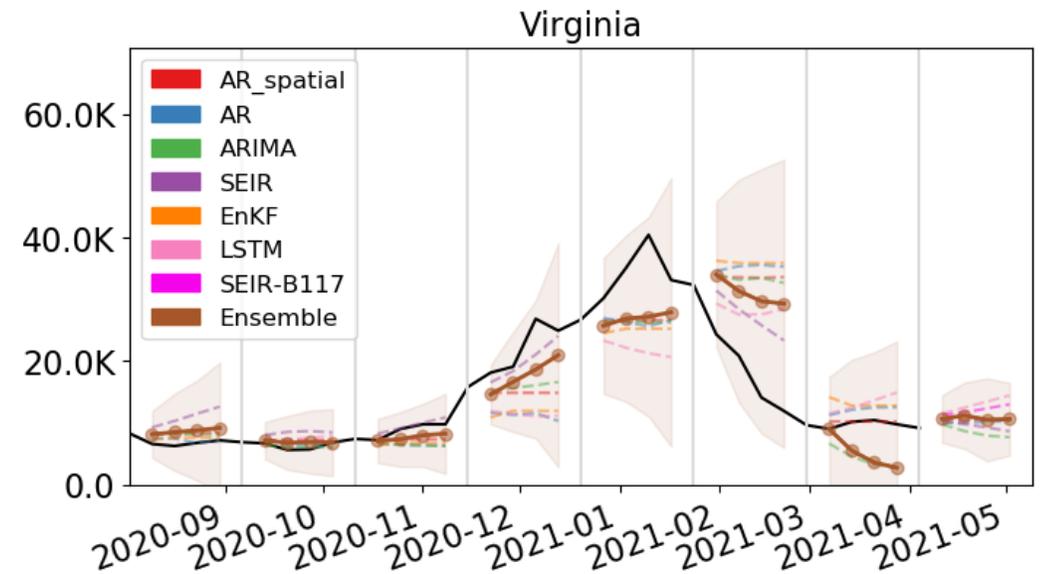
- Autoregressive (AR, ARIMA)
- Neural networks (LSTM)
- Kalman filtering (EnKF)

Weekly forecasts done at county level.

Models chosen because of their track record in disease forecasting and to increase diversity and robustness.

Ensemble forecast provides additional 'surveillance' for making scenario-based projections.

Also submitted to CDC Forecast Hub.



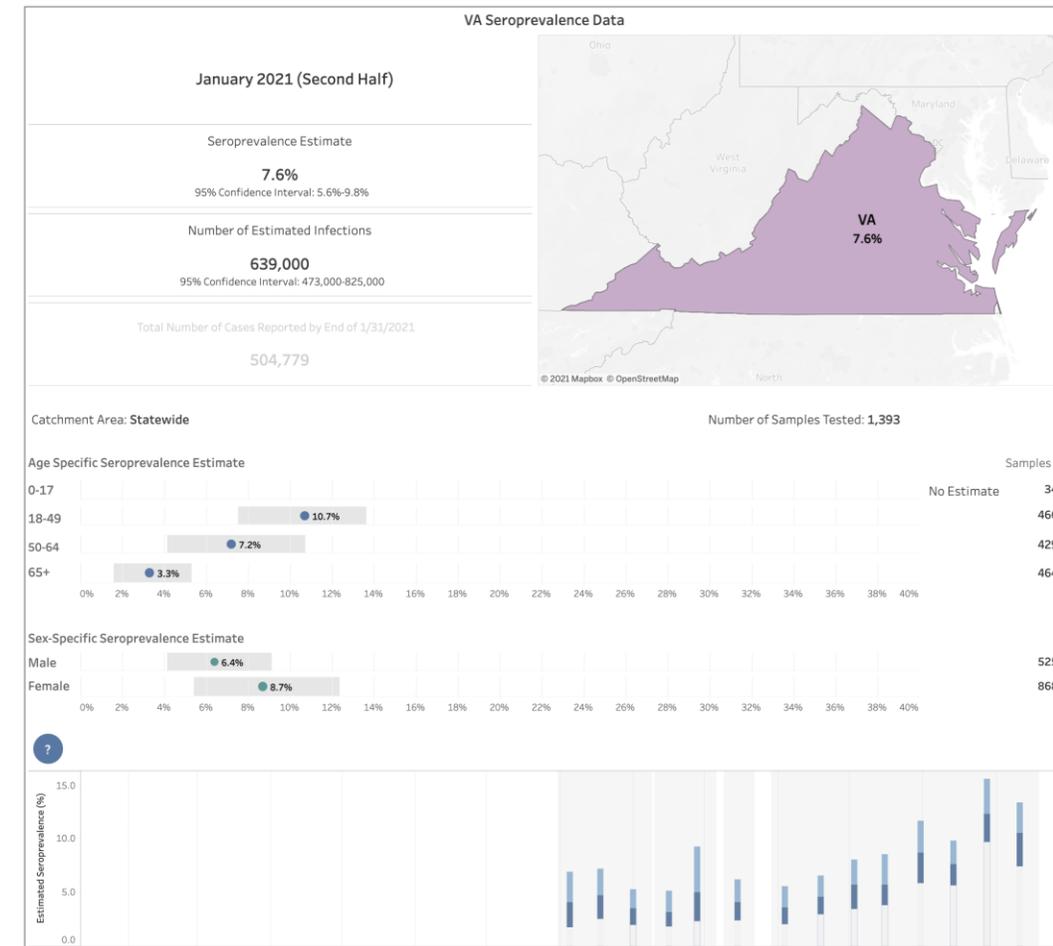
Seroprevalence updates to model design

Several seroprevalence studies provide better picture of how many actual infections have occurred

- CDC Nationwide Commercial Laboratory Seroprevalence Survey estimated 7.6% [5.6% – 9.8%] seroprevalence as of Jan 7th – 21st up from 5.7% a month earlier

These findings are equivalent to an ascertainment ratio of ~2x in the future, with bounds of (1.3x to 3x)

- Thus for 2x there are 2 total infections in the population for every confirmed case recently
- This measure now fully tracks the estimated ascertainment over time
- Uncertainty design has been shifted to these bounds (previously higher ascertainments as was consistent earlier in the pandemic were being used)



Calibration Approach

- **Data:**
 - County level case counts by date of onset (from VDH)
 - Confirmed cases for model fitting
- **Calibration:** fit model to observed data and ensemble's forecast
 - Tune transmissibility across ranges of:
 - Duration of incubation (5-9 days), infectiousness (3-7 days)
 - Undocumented case rate (1x to 7x) guided by seroprevalence studies
 - Detection delay: exposure to confirmation (4-12 days)
 - Approach captures uncertainty, but allows model to precisely track the full trajectory of the outbreak
- **Project:** future cases and outcomes generated using the collection of fit models run into the future
 - **Mean trend from last 14 days of observed cases and first week of ensemble's forecast used**
 - Outliers removed based on variances in the previous 3 weeks
 - 2 week interpolation to smooth transitions in rapidly changing trajectories

COVID-19 in Virginia:

Dashboard Updated: 4/13/2021
Data entered by 5:00 PM the prior day.

Cases, Hospitalizations and Deaths					
Total Cases*		Total Hospitalizations**		Total Deaths	
638,910		27,316		10,506	
(New Cases: 2,048) [^]					
Confirmed [†]	Probable [†]	Confirmed [†]	Probable [†]	Confirmed [†]	Probable [†]
497,840	141,070	25,878	1,438	8,811	1,695

* Includes both people with a positive test (Confirmed), and symptomatic with a known exposure to COVID-19 (Probable).
 ** Hospitalization of a case is captured at the time VDH performs case investigation. This underrepresents the total number of hospitalizations in Virginia.
[^]New cases represent the number of confirmed and probable cases reported to VDH in the past 24 hours.
[†] VDH adopted the updated CDC COVID-19 confirmed and probable surveillance case definitions on August 27, 2020. Found here: <https://wwwn.cdc.gov/nndss/conditions/coronavirus-disease-2019-covid-19/case-definition/2020/08/05/>

Outbreaks	
Total Outbreaks*	Outbreak Associated Cases
2,971	70,284

* At least two (2) lab confirmed cases are required to classify an outbreak.

Testing (PCR Only)	
Testing Encounters PCR Only*	Current 7-Day Positivity Rate PCR Only**
6,727,567	6.1%

* PCR* refers to "Reverse transcriptase polymerase chain reaction laboratory testing."
 ** Lab reports may not have been received yet. Percent positivity is not calculated for days with incomplete data.

Multisystem Inflammatory Syndrome in Children	
Total Cases*	Total Deaths
54	0

*Cases defined by CDC HAN case definition: <https://emergency.cdc.gov/han/2020/han00432.asp>

Accessed 8:30am April 14, 2021

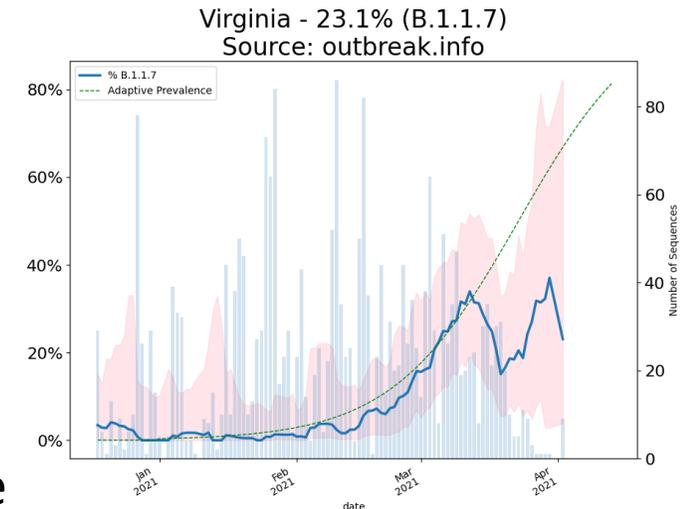
<https://www.vdh.virginia.gov/coronavirus/>

Scenarios – Transmission Control

- Variety of factors continue to drive transmission rates
 - Seasonal impact of weather patterns, travel and gatherings, fatigue and premature relaxation of infection control practices
- Plausible levels of transmission can be bounded by past experience
 - Assess transmission levels at the county level since May 1, 2020 through present
 - Use the highest and lowest levels experienced (excluding outliers) as plausible bounds for levels of control achievable
 - Transition from current levels of projection to the new levels over 2 months
- Projection Scenario:
 - **BestPast Control:** Lowest level of transmission (5th percentile)
 - **Fatigued Control:** Highest level of transmission (95th percentile) increased by additional 5%

Scenarios – Variant B.1.1.7

- New Variant B.1.1.7 is best understood and is in Virginia
 - **Transmission increase:** 50% increase from the current baseline projection based on estimated prevalence in past and future
 - **Increased Severity:** 60% increase in likelihood of hospitalization and a 60% increase in mortality [Nature](#)
 - **Emergence timing:** Gradual frequency increase reaching 50% frequency on April 5th, a couple weeks after the national estimate in [MMWR report from CDC](#) and refined by [Andersen et al.](#)
- Variant planning Scenario:
 - **DominantB117:** Current projected transmissibility continues to increase through June to a level 50% more transmissible

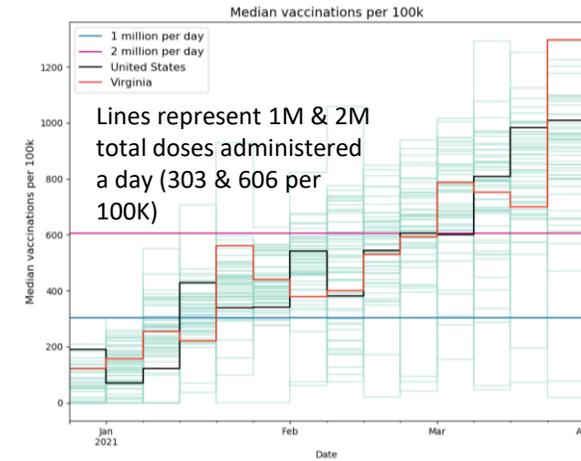


Estimated frequency from public genome repository with added analysis: 23%
Current frequency used in model: 59%

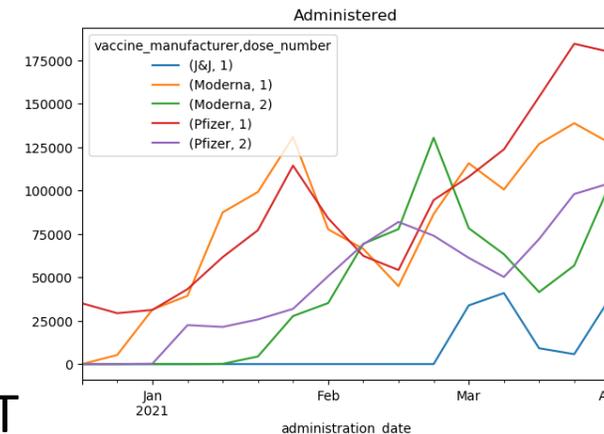


Scenarios – Vaccines

- Projected vaccine schedules constructed using current administration rates by dose and manufacturer for VA counties.
- Assumed vaccine efficacies
 - Pfizer/Moderna: 50% after first dose, 95% after second dose
 - J & J : 67% efficacy after first (and only) dose
 - Average 3.5 week gap between Pfizer/Moderna doses
 - Delay to efficacy from dose assumed to be 14 days
 - Immunity assumed to last duration of simulation ([NEJM study](#) shows long lasting, at least 7 months)
- Rapid administration pace will reach vaccine hesitancy thresholds more quickly
 - Pause in J&J administration assumed to be brief and NOT interrupt pace of administration



**All doses
(national)**



**Virginia doses
administered by
manufacturer**

Scenarios – Seasonal Effects and Vaccines

Three scenarios combine these seasonal effects and use the current vaccine schedule

- **Adaptive-DominantB117**: Boosting of transmissibility from the emergence and likely dominance of B.1.1.7
- **Adaptive-BestPast-DominantB117**: Best Past controls with transmission boost from B.1.1.7
- **Adaptive-FatigueControl-DominantB117**: Fatigued controls and transmission boost from B.1.1.7

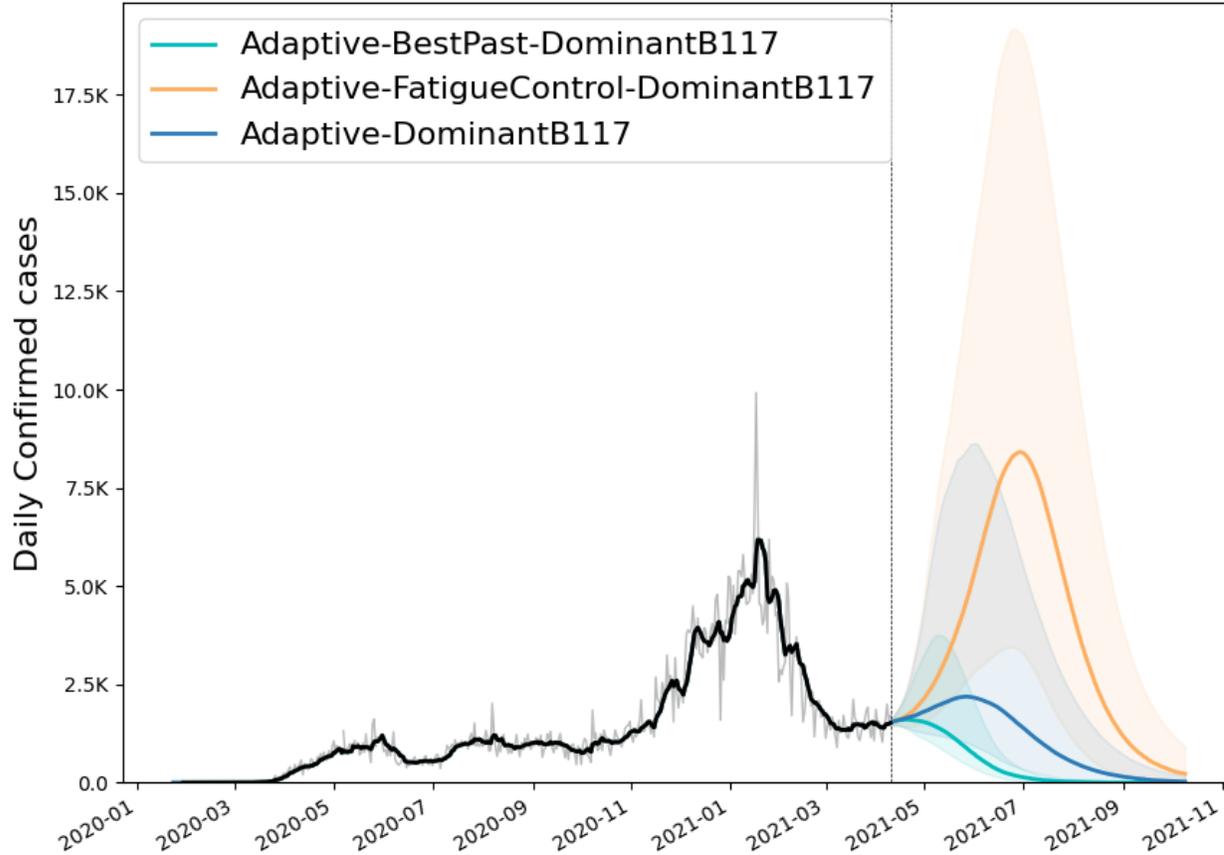
Counterfactuals with no vaccine (“NoVax”) are provided for comparison purposes

Model Results

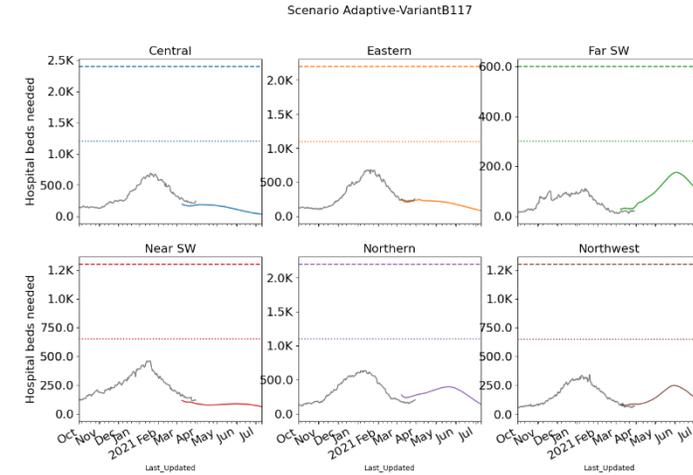
Outcome Projections

Confirmed cases

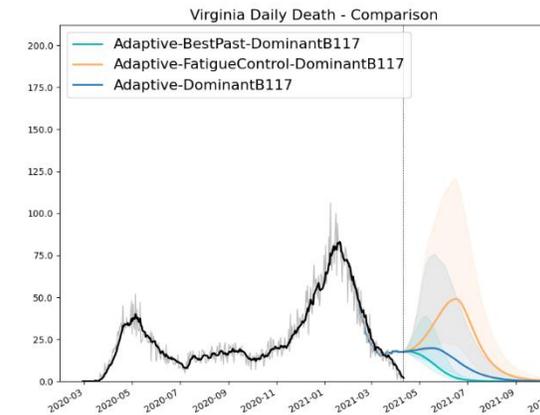
Virginia Daily Confirmed - Comparison



Estimated Hospital Occupancy

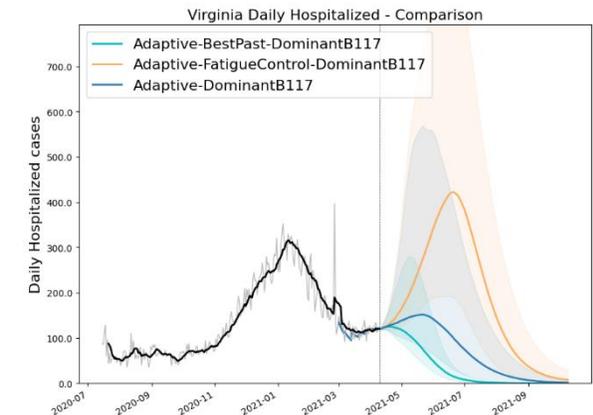


Daily Deaths



Death ground truth from VDH "Event Date" data, most recent dates are not complete

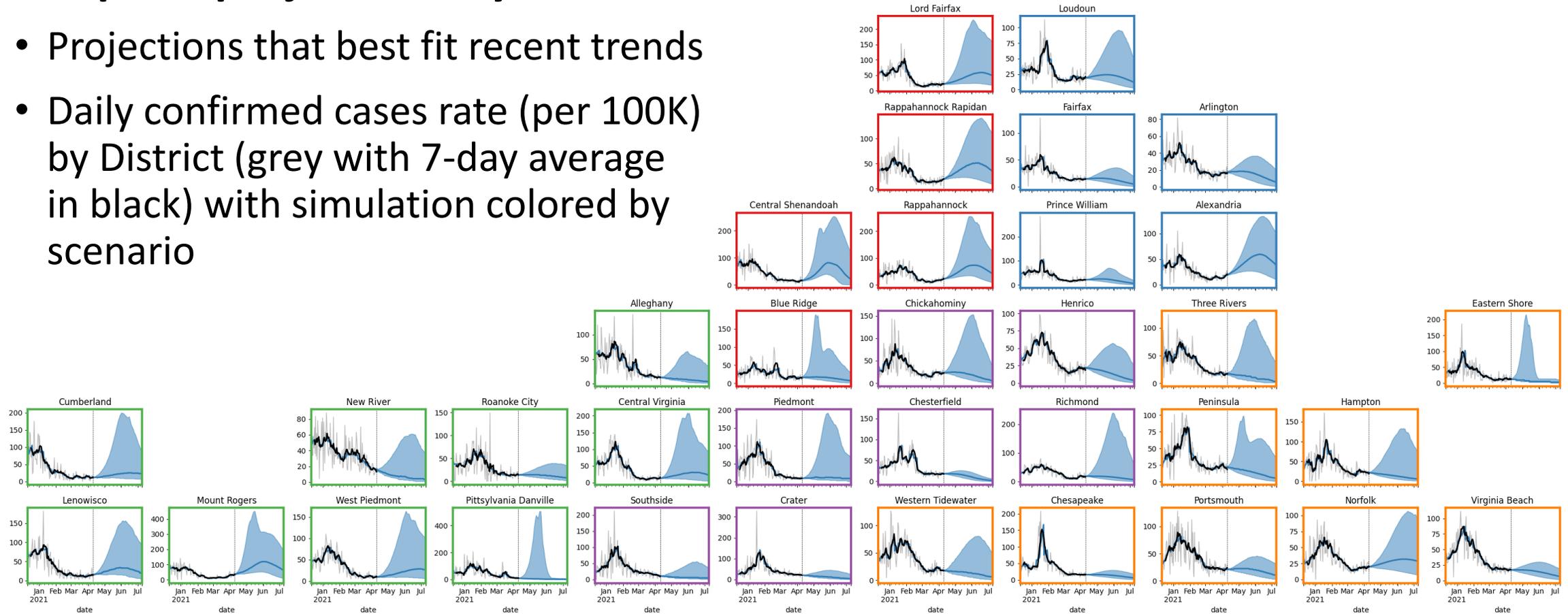
Daily Hospitalized



District Level Projections: Adaptive-DominantB117

Adaptive projections by District

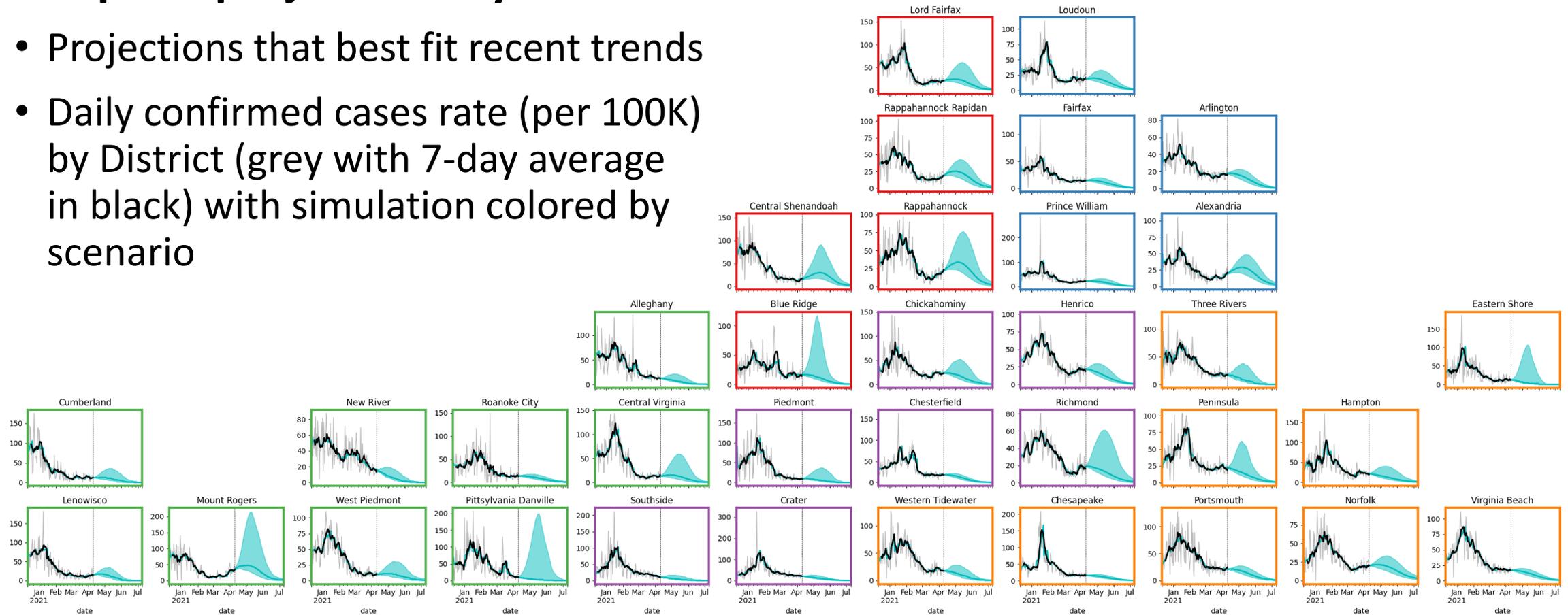
- Projections that best fit recent trends
- Daily confirmed cases rate (per 100K) by District (grey with 7-day average in black) with simulation colored by scenario



District Level Projections: Adaptive-BestPast-DominantB117

Adaptive projections by District

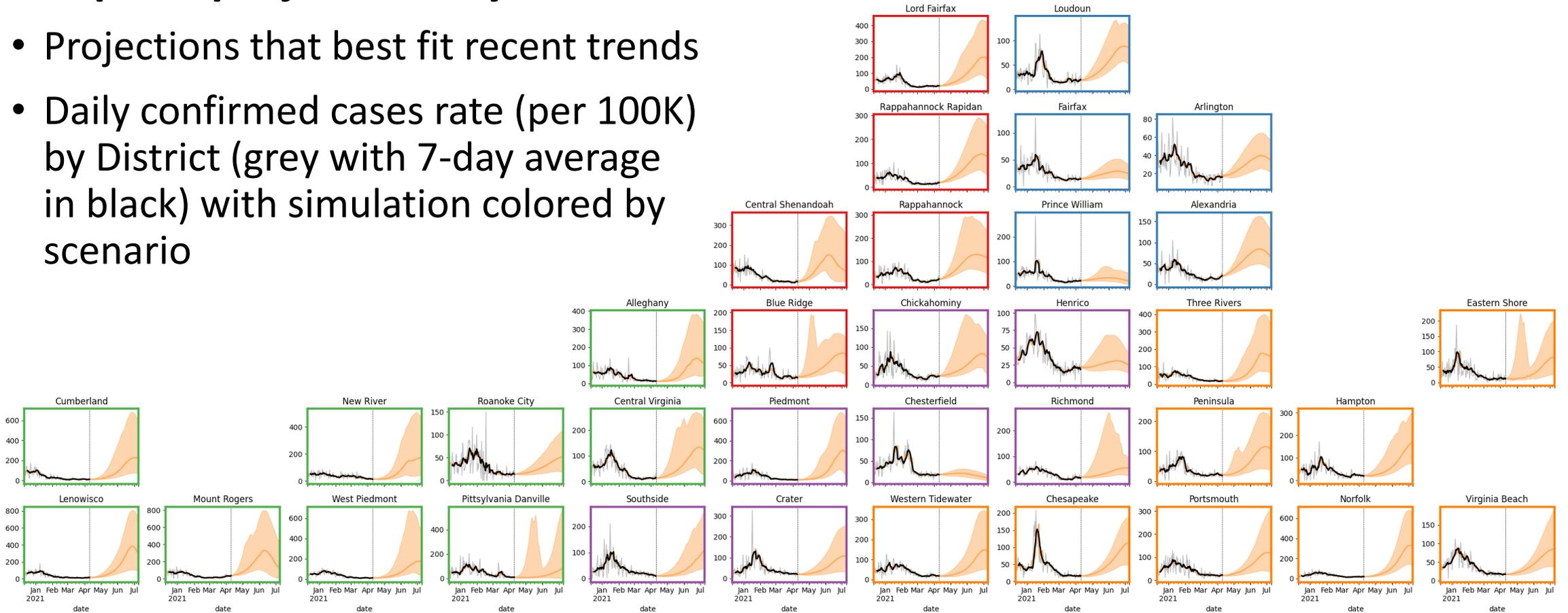
- Projections that best fit recent trends
- Daily confirmed cases rate (per 100K) by District (grey with 7-day average in black) with simulation colored by scenario



District Level Projections: Adaptive-FatigueControl-DominantB117

Adaptive projections by District

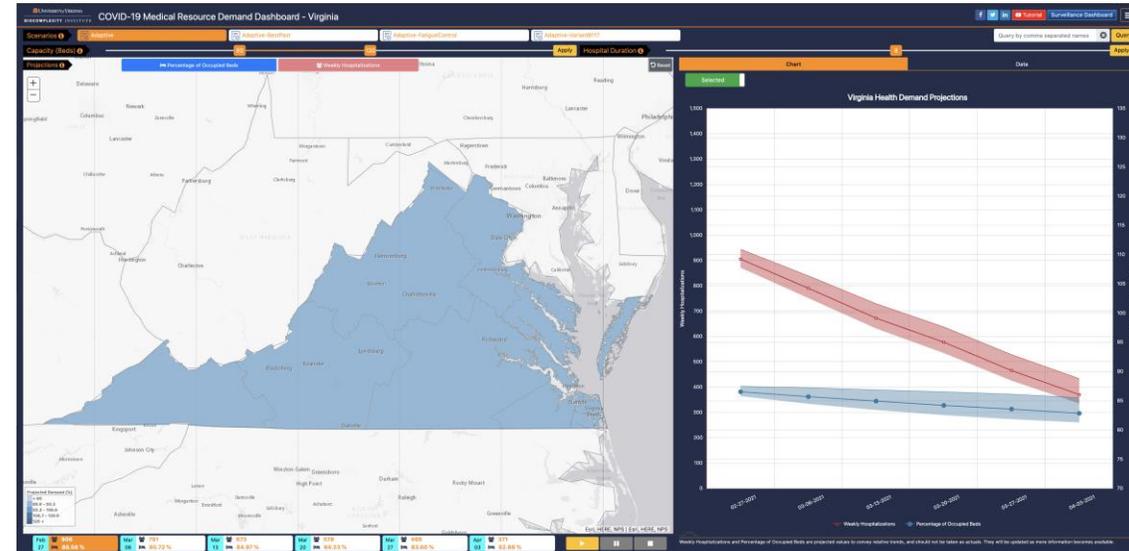
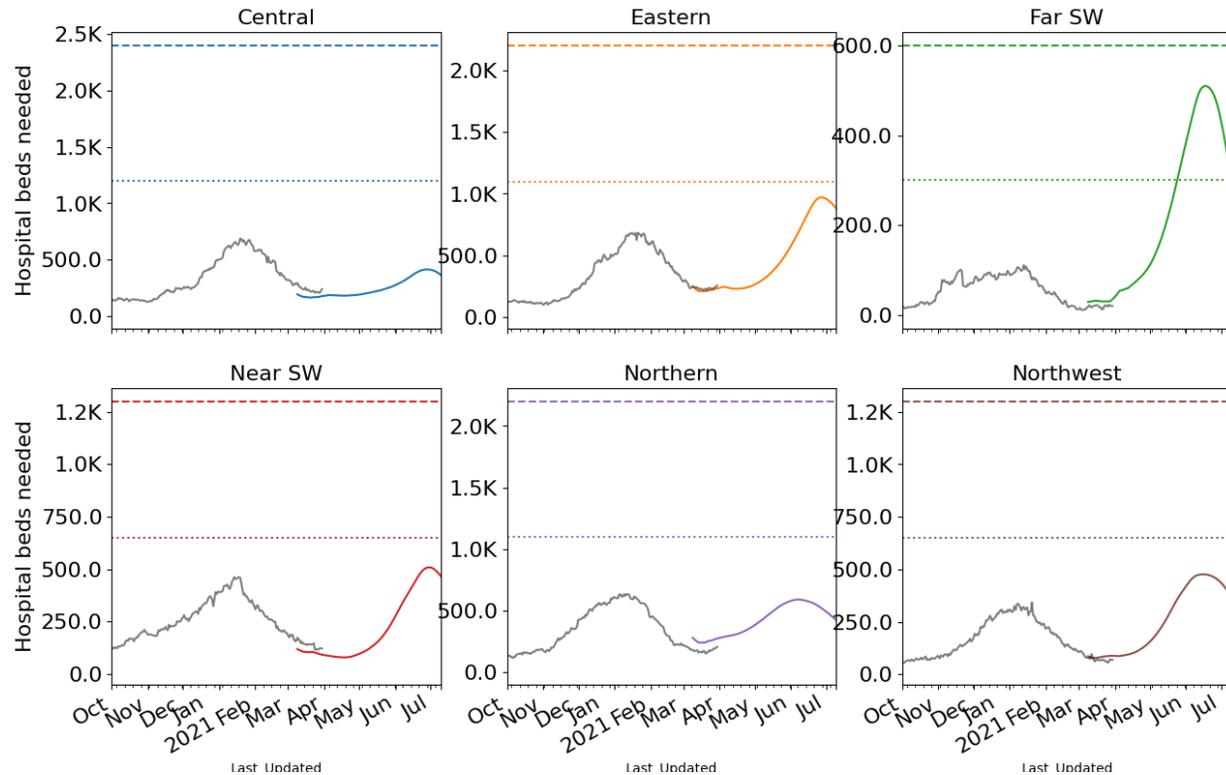
- Projections that best fit recent trends
- Daily confirmed cases rate (per 100K) by District (grey with 7-day average in black) with simulation colored by scenario



Hospital Demand and Bed Capacity by Region

Capacities* by Region – Adaptive-FatigueControl-DominantB117

COVID-19 capacity ranges from 80% (dots) to 120% (dash) of total beds



<https://nssac.bii.virginia.edu/covid-19/vmrddash/>

If Adaptive-FatigueControl-DominantB117 scenario:

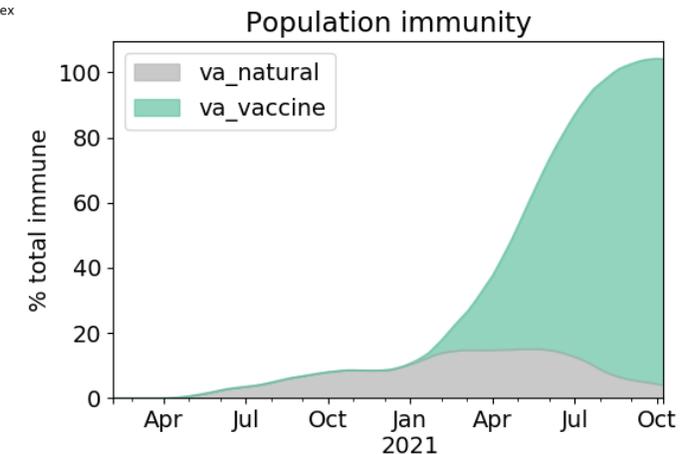
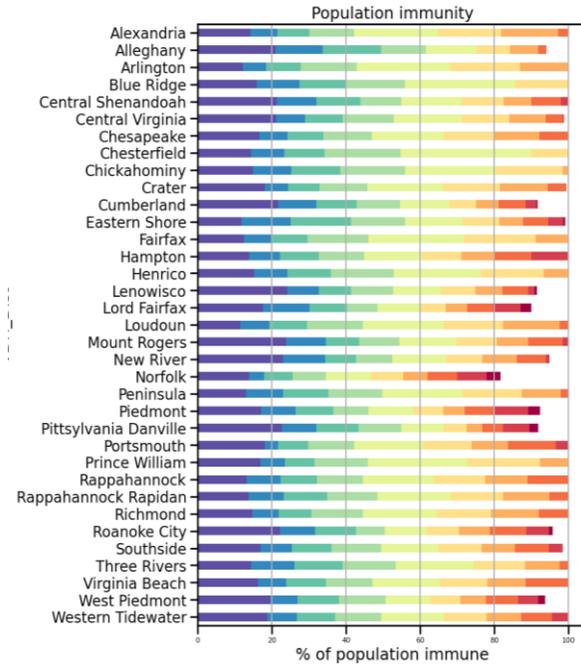
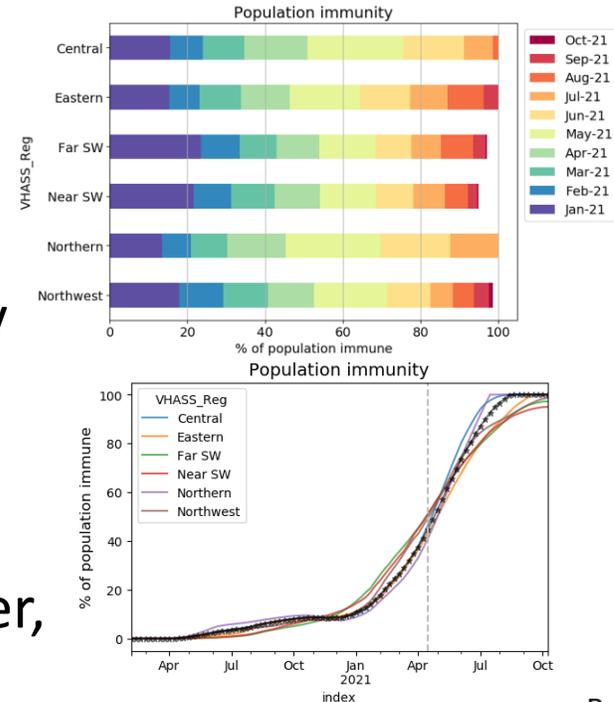
- Southwest initial bed capacity may be approached in late June

* Assumes average length of stay of 8 days
14-Apr-21

Virginia's Progress on Population Immunity

Natural Immunity and Vaccines combine to produce a population level of immunity

- How long immunity from infection with SARS-CoV2 lasts is not well understood but may vary based on severity of symptoms
 - We assume a conservative 6 month period of protection for these calculations
- Vaccine induced immunity is likely to last longer, we assume indefinite protection
 - This also assumes that all administered vaccines remain protective against current and future novel variants
- Population immunity depends on a very high proportion of the population getting vaccinated
 - Use regional vaccine acceptance



Key Takeaways

Projecting future cases precisely is impossible and unnecessary.

Even without perfect projections, we can confidently draw conclusions:

- **Case rates in Virginia have flattened with mix of growth and decline across districts**
- VA mean weekly incidence up to 19/100K from 16/100K, US up (21 from 19 per 100K)
- Progress remains stalled, with most counties at levels 2x the mean rate of Summer 2020
- Projections show slow growth overall across Commonwealth, boosted by B.1.1.7, but curtailed by vaccine
- Recent updates:
 - Modeled age-specific vaccinations past and future as well as severity of B.1.1.7 to drive outcome projections
 - Hospitalizations and deaths **reduced** by vaccination in ages most at risk for severe outcomes, but **increased** by prevalence of B.1.1.7
 - Scenarios adjusted to reflect increasing dominance of B.1.1.7 and return of the Best of Past control scenario
 - Regional vaccine acceptance integrated into projections
- The situation continues to change. Models continue to be updated regularly.

References

Venkatramanan, S., et al. "Optimizing spatial allocation of seasonal influenza vaccine under temporal constraints." *PLoS Computational Biology* 15.9 (2019): e1007111.

Arindam Fadikar, Dave Higdon, Jiangzhuo Chen, Bryan Lewis, Srinivasan Venkatramanan, and Madhav Marathe. Calibrating a stochastic, agent-based model using quantile-based emulation. *SIAM/ASA Journal on Uncertainty Quantification*, 6(4):1685–1706, 2018.

Adiga, Aniruddha, Srinivasan Venkatramanan, Akhil Peddireddy, et al. "Evaluating the impact of international airline suspensions on COVID-19 direct importation risk." *medRxiv* (2020)

NSSAC. PatchSim: Code for simulating the metapopulation SEIR model. <https://github.com/NSSAC/PatchSim>

Virginia Department of Health. COVID-19 in Virginia. <http://www.vdh.virginia.gov/coronavirus/>

Biocomplexity Institute. COVID-19 Surveillance Dashboard. <https://nssac.bii.virginia.edu/covid-19/dashboard/>

Google. COVID-19 community mobility reports. <https://www.google.com/covid19/mobility/>

Biocomplexity page for data and other resources related to COVID-19: <https://covid19.biocomplexity.virginia.edu/>

Questions?

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Supplemental Slides

Weekly Cases and Hospitalizations

Weekly confirmed cases

Week Ending	Adaptive-Dominant B117	Adaptive-BestPast-Dominant B117	Adaptive-Fatigued Control-Dominant B117
4/11/21	10,297	10,297	10,298
4/18/21	11,121	11,064	11,194
4/25/21	11,670	11,165	12,350
5/2/21	12,398	10,882	14,361
5/9/21	13,285	10,236	17,256
5/16/21	14,160	9,176	21,192
5/23/21	14,936	7,768	26,222
5/30/21	15,257	6,144	32,305
6/6/21	14,928	4,566	39,599
6/13/21	14,185	3,182	47,166
6/20/21	13,046	2,093	53,706
6/27/21	11,438	1,402	57,674

Weekly Hospitalizations

Week Ending	Adaptive-Dominant B117	Adaptive-BestPast-Dominant B117	Adaptive-Fatigued Control-Dominant B117
4/11/21	830	830	830
4/18/21	868	863	874
4/25/21	908	869	962
5/2/21	953	836	1,107
5/9/21	1,002	770	1,305
5/16/21	1,039	672	1,559
5/23/21	1,058	552	1,858
5/30/21	1,033	422	2,174
6/6/21	960	302	2,494
6/13/21	864	203	2,755
6/20/21	755	128	2,924
6/27/21	632	83	2,898

Date of Onset Reproductive Number

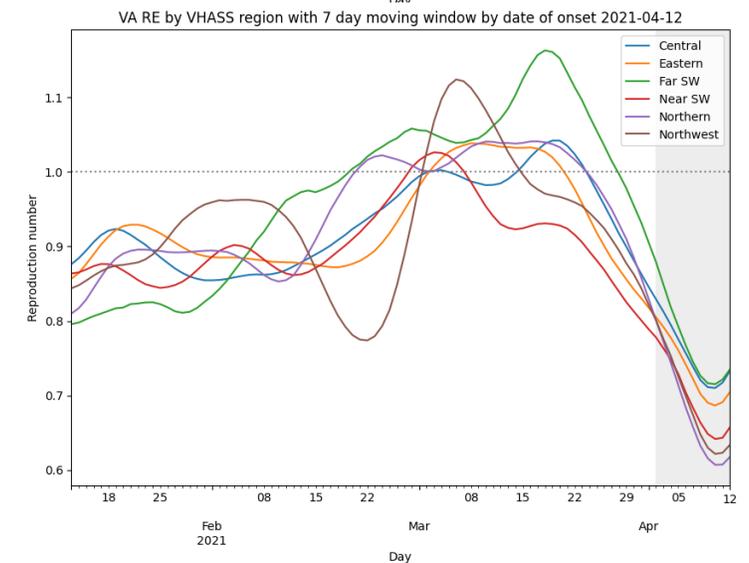
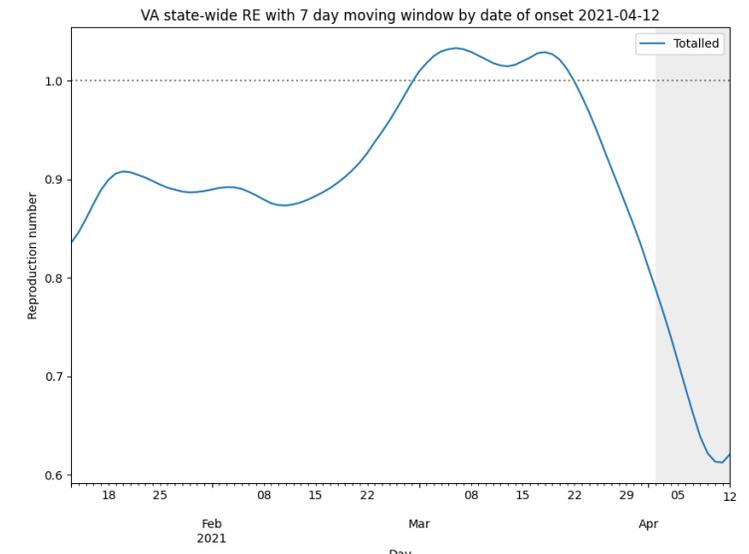
April 3rd Estimates

Region	Date of Onset R_e	Date Onset Diff Last Week
State-wide	0.765	0.045
Central	0.813	0.003
Eastern	0.792	0.049
Far SW	0.849	0.051
Near SW	0.763	0.057
Northern	0.773	-0.005
Northwest	0.776	0.020

Methodology

- Wallinga-Teunis method (EpiEstim¹) for cases by **confirmation date**
- Serial interval: updated to discrete distribution from observations (mean=4.3, Flaxman et al, Nature 2020)
- Using Confirmation date since due to increasingly unstable estimates from onset date due to backfill

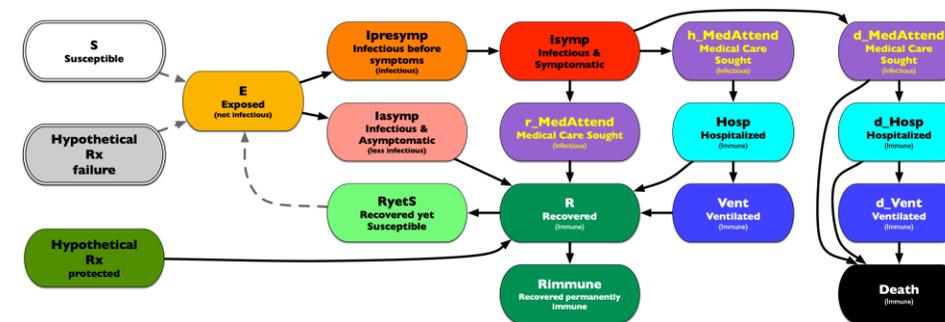
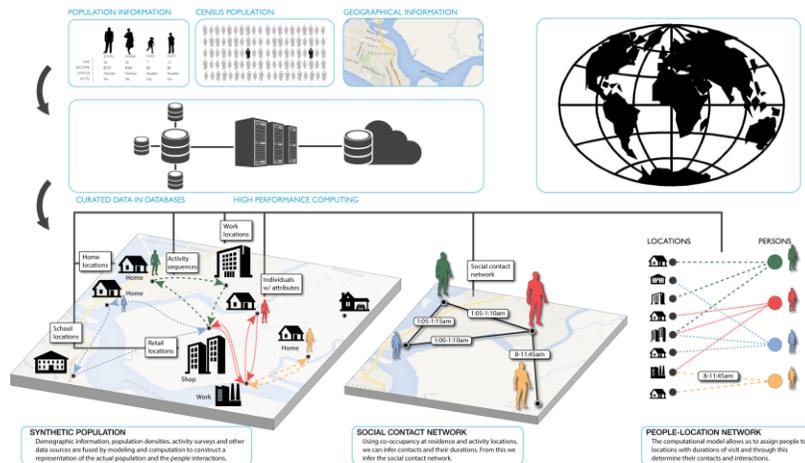
1. Anne Cori, Neil M. Ferguson, Christophe Fraser, Simon Cauchemez. A New Framework and Software to Estimate Time-Varying Reproduction Numbers During Epidemics. American Journal of Epidemiology, Volume 178, Issue 9, 1 November 2013, Pages 1505–1512, <https://doi.org/10.1093/aje/kwt133>



Agent-based Model (ABM)

EpiHiper: Distributed network-based stochastic disease transmission simulations

- Assess the impact on transmission under different conditions
- Assess the impacts of contact tracing



Detailed Disease Course of COVID-19

- Literature based probabilities of outcomes with appropriate delays
- Varying levels of infectiousness
- Hypothetical treatments for future developments

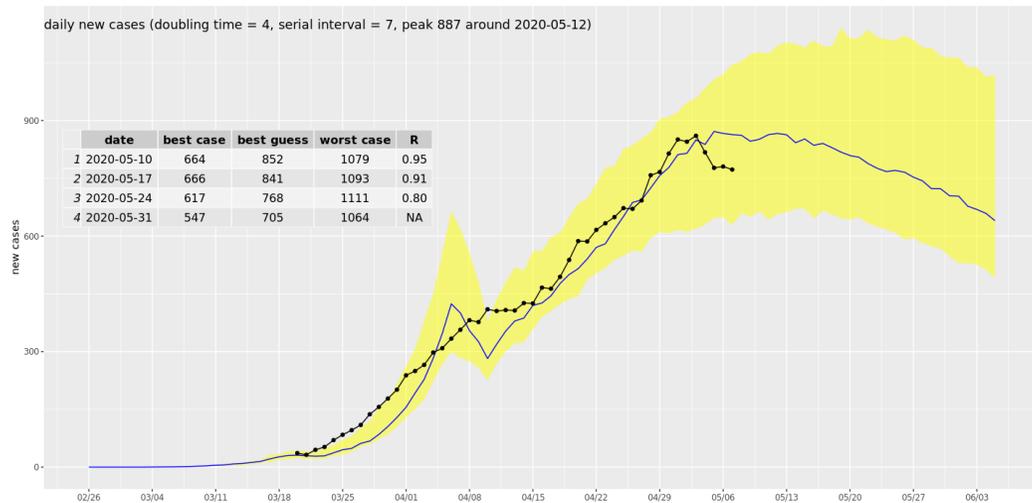
Synthetic Population

- Census derived age and household structure
- Time-Use survey driven activities at appropriate locations

ABM Social Distancing Rebound Study Design

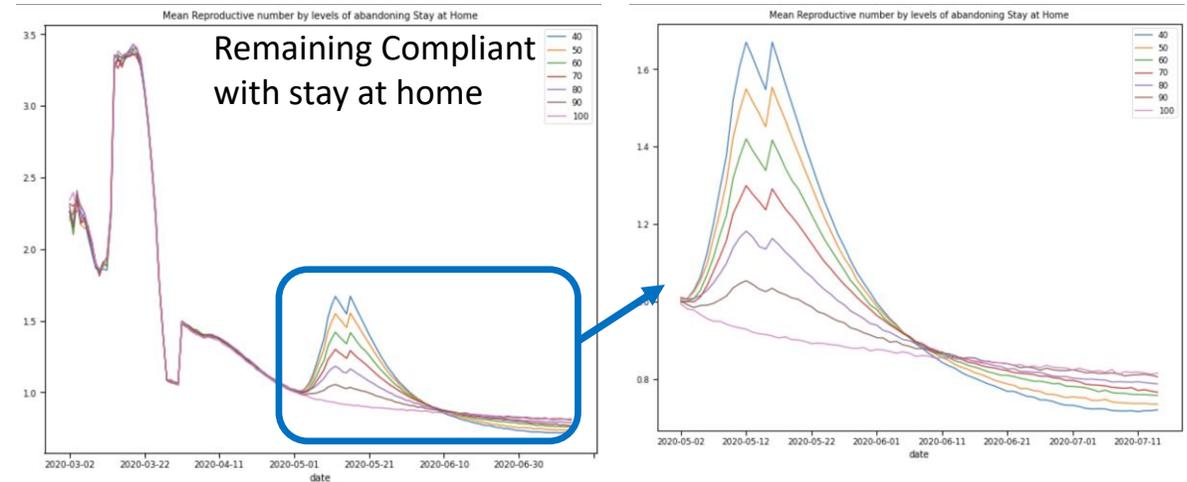
Study of "Stay Home" policy adherence

- Calibration to current state in epidemic
- Implement "release" of different proportions of people from "staying at home"



Calibration to Current State

- Adjust transmission and adherence to current policies to current observations
- For Virginia, with same seeding approach as PatchSim



Impacts on Reproductive number with release

- After release, spike in transmission driven by additional interactions at work, retail, and other
- At 25% release (70-80% remain compliant)
- Translates to 15% increase in transmission, which represents a $1/6^{\text{th}}$ return to pre-pandemic levels